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(54) Title: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE THEREOF (57) Abstract A novel lymphocyte receptor protein, its DNA sequence, and its role in the calcium activation pathway is described. The protein, or genetically engineered constructs encoding it, are shown to increase lymphocyte response, and to identify ligands of the protein receptor. Antibodies to the proteins of the invention are generated for diagnostic therapeutics. The protein and DNA can also be used for diagnostic purposes and for identifying agents for modulating the calcium induced activation pathway. A particular advantage of the present invention is that it provides lymphocyte activation of receptor found on all B cells, but only on a subset of T cells. The receptor can thus be targeted to specifically regulate B cell responses without affecting mature T cell activity. Such targeting specificity is always advantageous, particularly where an increase or decrease of antibody production is desired, e.g., during an infection (increase) or to avoid immune complex deposition complications (rheumatoid arthritis, glomerulonephritis, and other autoimmune conditions).		

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**A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS CAML, NUCLEIC ACIDS
ENCODING THE SAME AND METHODS OF USE THEREOF**

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FIELD OF THE INVENTION

The invention relates generally to the regulation of transcription in lymphocytes, proteins
involved therein, antibodies thereof, nucleic acids that encode the proteins and uses of the
nucleic acids, antibodies and proteins.

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BACKGROUND OF THE INVENTION

Investigators are only beginning to unravel the mechanisms that control the cellular
response to extrinsic factors. One basic feature of many of such mechanisms is the initial
20 binding of an extrinsic factor, *e.g.*, a ligand, to a cell surface membrane protein, *i.e.*, a
receptor. The binding of a ligand to its receptor usually effects a cellular change through
a cascade of events. These events commonly involve other proteins, such as protein
kinases, protein phosphatases, JAK proteins, Stat proteins, and/or G-proteins. In addition,
there is generally a requirement for a transcription factor to bind to a specific DNA
25 regulatory sequence in the nucleus of the cell, and thereby initiate the transcription of one
or more particular genes.

Other factors are often involved. In antigen-stimulated lymphocyte activation, for
example, calcium (Ca^{2+}) influx is also necessary for the ultimate initiation of DNA
30 transcription. The increased cytoplasmic calcium concentration may originate as an
external influx or a release of internal stores. Increased calcium concentration which
activates the calcium-dependent protein phosphatase calcineurin acts in conjunction with
other agents to signal the initiation of transcription. It is clear that the pathway involving
calcium influx is essential to a number of processes involved with activation and

proliferation of cells.

- Intracellular calcium levels play a major function in a number of different cell types involving a number of different activities. In addition to the induction of gene
- 5 transcription by calcium influx, many other calcium-dependent events, such as those which occur during muscle contraction (both cardiac and skeletal), vesicle degranulation (such as in the response of neutrophils and macrophages to infection, or basophil response to antigen stimulation, or release of acetylcholine by neurons), and closure of intracellular gap junctions offer opportunities for cellular regulation. The cell cycle can also involve
- 10 fluxes of calcium. Intracellular chelators which block changes in intracellular calcium concentration can block the cell cycle from progressing, thereby arresting cell division. [Rabinovich *et al.*, *J. of Immunol.*, 137:952-961 (1986)]. Therefore, regulation of calcium can be effective in modulating cell division in normal and diseased cells.
- 15 Lymphocytes are a primary component of the cellular arm of the immune system. Activation of one particular type of lymphocyte, a T-cell, can result through the stimulation of a T-cell receptor by *e.g.*, the binding of a T-cell receptor (TCR) to an antigen presented by an antigen-presenting cell. This stimulation results in the activation a Ca^{2+} -dependent phosphatase, calcineurin. Activated calcineurin, in turn, activates NF-AT,
- 20 a lymphocyte specific transcription factor that together with a companion transcription factor, AP-1, effects the expression of the inducible T-cell growth factor, interleukin-2 (IL-2). Activation of AP-1 is a calcium-independent process that involves protein kinase C, and can be experimentally achieved with the addition of phorbol myristate acetate (PMA). The immunosuppressant drug cyclosporin A (CsA) binds to and inhibits the
- 25 prolyl isomerase activity of cyclophilin and the resulting drug-isomerase complex inactivates calcineurin, by a direct interaction near the active site of the enzyme. [Liu *et al.*, *Cell*, 66:807-15 (1991)]; [Clipstone and Crabtree, *Nature*, 357:695-7 (1992)]; [O'Keefe *et al.*, *Nature*, 357:692-4 (1992)]. NF-KB is a third key transcription factor which is important in the activation of lymphocytes and which is activated following the
- 30 stimulation of the T-cell or B-cell antigen receptor.

Another protein associated with the calcium signaling pathway in lymphocytes is the recently identified calcium-signal modulating cyclophilin ligand (CAML) [Bram, R. J. and Crabtree, G. R., *DNA Encoding Calcium-Signal Modulating Cyclophilin Ligand*, U.S.

Patent No. 5,523,227, Issued June 4, 1996, hereby incorporated by reference in its entirety]. CAML binds cyclophilin B with reasonable specificity, i.e., CAML does not bind cyclophilin A or C. Unlike the cyclosporin A-cyclophilin complex, however, the CAML-cyclophilin B complex does not directly bind to calcineurin. Thus CAML appears to affect calcineurin through its regulation of Ca^{2+} influx. As expected, CsA can indirectly block the activating effect of CAML on transcription, by inhibiting calcineurin. In addition, CAML appears to have no effect on the activation of AP-1, and so the CAML-dependent activation of NF-AT experimentally requires the addition of PMA.

CAML acts downstream from an extrinsic signal but upstream from calcineurin. The location of CAML in cytoplasmic vesicles suggests that it can regulate Ca^{2+} influx by modulating intracellular Ca^{2+} release. However, there remains a need to determine the natural factor (or factors) that communicate the external signal to the cellular CAML. Further, there is a need to understand how CAML interacts with this factor in order to learn how to better control the important cellular processes that CAML helps to regulate. A different class of signaling molecule is the TNFR family of cell surface receptors [Smith *et al.*, *Cell* 76:959-62 (1994)]. These receptors initiate intracellular signals leading to the onset of cell growth, death, or gain of effector function.

20

SUMMARY OF THE INVENTION

A novel lymphocyte receptor, its DNA sequence, and its role in the calcium activation pathway is described. The protein, or genetically engineered constructs encoding it, can be used to enhance lymphocyte response, or to identify ligands of the protein receptor.

The soluble, extracellular domain can be used to inhibit cellular activation. Antibodies to the protein can be generated for diagnostic or therapeutic uses. The protein and DNA may also be used for diagnostic purposes and for identifying agents for modulating the calcium induced activation pathway. Knowledge of the coding sequence allows for manipulation of cells to elucidate the mechanism of which CAML is a part.

A particular advantage of the present invention is that it provides lymphocyte activation of a receptor found on all B cells, but only on a subset of T cells. The receptor can thus be targeted to specifically regulate B cell responses without affecting mature T cell activity. Such targeting specificity is always advantageous, particularly where an increase or

decrease of antibody production independent of cellular immune responses is desired, *e.g.*, during an infection (increase) or to avoid immune complex deposition complications (rheumatoid arthritis, glomerulonephritis, and other autoimmune conditions).

- 5 Crosslinking the novel cell surface receptor of the present invention activates B cells and some populations of T cells. Activation of these cells increases the immune system activity. On the other hand, blocking or inhibiting the novel cell surface receptor of the present invention can result in immunosuppression. Depending on the endogenous level of activation of the receptor, which can be evaluated using the antibodies or nucleic acids
10 of the invention, receptor activity can be enhanced or suppressed to achieve a desired outcome. Either activating or inhibiting the function of the novel cell surface receptor of the present invention can be used to treat cancers of T and B cells.

- The present invention includes an isolated Transmembrane Activator and CAML-Interactor
15 (TACI) protein that functions as a cell surface signaling protein and comprises an extracellular domain, a membrane spanning segment, and a cytoplasmic domain. In one embodiment, the TACI protein is a plasma membrane receptor in which the extracellular domain resides at the N-terminal portion of the protein and the cytoplasmic domain resides at the C-terminal portion of the protein. The N-terminal portion of the TACI protein
20 functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the C-terminal portion of the TACI protein to the N-terminal domain of CAML. Since CAML is an integral membrane protein that is localized to cytoplasmic vesicles, the TACI protein is a plasma membrane receptor that directly interacts with an intracellular organelle in lymphocytes.

- 25 In one embodiment, the monomeric form of the isolated TACI protein consists of about 295 amino acids. In a preferred embodiment the monomeric form of a Transmembrane Activator and CAML Interactor (TACI) protein contains 280 to 310 amino acids. In more preferred embodiments the monomeric form of a TACI protein contains 290 to 296 amino
30 acids. In a specific embodiment exemplified *infra*, the monomeric form of a TACI protein contains 293 amino acids.

One embodiment of the isolated TACI protein contains two TNFR superfamily cysteine-rich repeats [Bairoch, *Nucl. Acids Res.*, 21:3097-3103 (1993)]. In a preferred

embodiment, a TACI protein that is appropriately stimulated, *in situ*, such as by a ligand or an anti-TACI antibody, initiates the activation of a transcription factor through the combination of a Ca^{2+} -dependent pathway and a Ca^{2+} -independent pathway.

- 5 The present invention includes an isolated nucleic acid that consists of at least 18 nucleotides of a nucleotide sequence that has at least 60% similarity with SEQ ID NO:1, or alternatively at least 60% similarity with the coding sequence of SEQ ID NO:1. The nucleotide sequence encodes a TACI protein which has a binding affinity for CAML. In one such embodiment the isolated nucleic acid encodes a TACI protein.
- 10 In a preferred embodiment of the present invention the nucleotide sequence has at least 75% similarity with SEQ ID NO:1, or has at least 75% similarity with the coding sequence of SEQ ID NO:1. In a more preferred embodiment, the nucleotide sequence has at least 90% similarity with SEQ ID NO:1, or has at least 90% similarity with the coding
- 15 sequence of SEQ ID NO:1. In an even more preferred embodiment, the nucleotide sequence has between 95-98% similarity with SEQ ID NO:1, or has between 95-98% similarity with the coding sequence of SEQ ID NO:1. In a particular embodiment the nucleotide sequence is SEQ ID NO:1. In a related embodiment, the nucleotide sequence consists of the coding sequence of SEQ ID NO:1. In a specific embodiment, exemplified
- 20 *infra*, the isolated nucleic acid has the nucleotide sequence of SEQ ID NO:1. In a related embodiment, the isolated nucleic acid consists of the coding sequence of SEQ ID NO:1.

- In another related embodiment the present invention includes an isolated nucleic acid which contains at least 18 nucleotides and hybridizes to SEQ ID NO:1, or more
- 25 particularly hybridizes to the coding sequence of SEQ ID NO:1. In one such embodiment, the hybridization is performed under moderate stringency. In another embodiment, the hybridization is performed under standard hybridization conditions. In yet a third embodiment, the hybridization is performed under stringent hybridization conditions.

- 30 In still another related embodiment the present invention includes an isolated nucleic acid which contains at least 18 nucleotides of a nucleotide sequence that encodes a TACI protein having an amino acid sequence of either SEQ ID NO:2, or SEQ ID NO:2 with one or more conservative substitutions. In one such embodiments of this type, the isolated

nucleic acid encodes an N-terminal fragment of the TACI protein corresponding to the extracellular domain. In another embodiment, the isolated nucleic acid encodes a C-terminal fragment of the TACI protein that is sufficient to bind to the N-terminal 146 amino acids of CAML. In yet another embodiment, the isolated nucleic acid encodes the transmembrane portion of the TACI protein. In still another embodiment, the isolated nucleic acid encodes the full-length TACI protein.

In a preferred embodiment of the present invention, the isolated nucleic acid consists of at least 24 nucleotides. In a more preferred embodiment, the isolated nucleic acid consists of at least 30 nucleotides. In an even more preferred embodiment, the isolated nucleic acid consists of at least 36 nucleotides. Oligonucleotides of the invention can be used as nucleic acid probes, PCR primers, antisense nucleic acids, and the like, for diagnostic and therapeutic purposes.

In one embodiment of the present invention, an isolated nucleic acid encodes a C-terminal fragment of the TACI protein that is sufficient to bind to the N-terminal 146 amino acids of CAML. In one particular embodiment of this type, the C-terminal fragment contains about 126 amino acids. In another embodiment of this type the C-terminal fragment has an amino acid sequence of either SEQ ID NO:4, or SEQ ID NO:4 with one or more conservative substitutions.

In another embodiment, the isolated nucleic acid encodes an N-terminal fragment of the CAML-binding protein corresponding to the extracellular domain. In a particular embodiment of this type the N-terminal fragment has an amino acid sequence of either SEQ ID NO:6, or SEQ ID NO:6 with one or more conservative substitutions.

In a preferred embodiment, the isolated nucleic acid encodes a TACI protein that has a binding affinity for CAML. When such a TACI protein is appropriately stimulated, *in situ*, it initiates activation of a transcription factor through the combination of a Ca^{2+} -dependent pathway and a Ca^{2+} -independent pathway. In a more preferred embodiment, the isolated nucleic acid encodes a TACI protein having the amino acid sequence of SEQ ID NO:2.

The present invention also includes a DNA construct comprising an isolated nucleic acid

of the present invention that is a recombinant DNA operatively linked to an expression control sequence. The expression control sequence can be selected from the group consisting of the early or late promoters of SV40 or adenovirus, the *lac* system, the *trp* system, the *TAC* system, the *TRC* system, the major operator and promoter regions of
5 phage λ , the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase, the promoters of acid phosphatase and the promoters of the yeast α -mating factors.

In a preferred embodiment, the expression control sequence is either a standard tet inducible promoter, a metallothionein promoter, or an ecdysone promoter. In a more
10 preferred embodiment, the expression control sequence is the SR_{α} promoter.

The present invention also includes a unicellular host transformed with a recombinant DNA construct of the present invention. In one embodiment the unicellular host is a prokaryote. In another embodiment the unicellular host is a eukaryote. Preferably the
15 eukaryotic host is a mammalian cell, for example, a COS, CHO or Jurkat T cell, which could be useful for evaluating activity of the TACI protein or to identify modulatory agents.

The present invention includes the isolated polypeptides encoded by the nucleic acids of
20 the present invention, fragments thereof, and fusion proteins thereof. In one embodiment, the polypeptide fragment consists of an N-terminal fragment of the TACI protein corresponding to the regulatory extracellular domain. In a particular embodiment the N-terminal fragment has an amino acid sequence of SEQ ID NO:6 or SEQ ID NO:6 with one or more conservative substitutions.

25

In another embodiment, the polypeptide fragment consists of a C-terminal fragment of the TACI protein that is sufficient to bind to the N-terminal 146 amino acids of CAML. In one such embodiment, the C-terminal fragment contains 95 to 130 amino acids. In a specific embodiment, the C-terminal fragment contains the C-terminal 126 amino acids of
30 SEQ ID NO:2. In an alternative embodiment the C-terminal fragment of the TACI protein contains about 110 amino acids. In a preferred embodiment of this type, the C-terminal fragment contains 107 amino acids and has an amino acid sequence of SEQ ID NO:4.

The present invention also includes the preparation of a recombinant form of the extracellular portion of a TACI protein, thereby creating a dominant-negative or blocking reagent. This component intercepts the normal endogenous ligands which serve to crosslink and activate the TACI protein. Administration of such a polypeptide acts to
5 suppress the immune system. Such administration is useful in the treatment or prevention of autoimmune disease or graft-rejection or graft-vs-host disease following transplantation.

A chimeric TACI protein of the invention may be a protein that is generated by joining the extracellular domain of another receptor molecule with a transmembrane domain and
10 the intracellular domain of a TACI protein. In another embodiment, the extracellular domain of a TACI protein can be joined with a transmembrane domain and an intracellular domain of another receptor molecule. The transmembrane domain can be the transmembrane domain of a TACI protein, the transmembrane domain of the other receptor, or a different transmembrane domain. Preferably, the transmembrane domain is
15 from the same protein component of the chimera as the extracellular domain.

In a preferred embodiment the polypeptide is a TACI protein encoded by a nucleic acid of the present invention that has a binding affinity for CAML and when appropriately stimulated, *in situ*, initiates activation of a transcription factor through the combination of
20 a Ca^{2+} -dependent pathway and a Ca^{2+} -independent pathway.

The present invention also includes antisense nucleic acids that hybridize under physiological conditions to the mRNAs that encode the TACI proteins of the present invention. Such antisense nucleic acids may be RNA transcribed from an antisense gene,
25 or RNA or DNA produced exogenously (whether by expression or chemical synthesis). Preferably, a synthetic antisense nucleic acid is prepared with non-naturally occurring bonds to prevent its rapid hydrolysis and thus increase its effective half-life.

A knockout animal is also part of the present invention. The knockout animal comprises a
30 first and second allele which each naturally encode and express functional TACI protein but in which at least one of the two alleles is defective and thereby prevents the animal from expressing an adequate amount of the TACI protein. In one embodiment of this type, the first allele contains a defect that prevents the animal from expressing any functional TACI protein. In a preferred embodiment, a knockout animal contains both a

defective first allele and a defective second allele. These defective alleles prevent the animal from expressing functional TACI protein. In a preferred embodiment, the knockout animal is a knockout mouse.

5 The present invention also includes antibodies to all of the nucleic acids and polypeptides of the present invention. In a specific embodiment, the antibody is prepared against the TACI protein having an amino acid sequence of SEQ ID NO:2, or an antigenic fragment thereof. The antibodies of the present invention can be either monoclonal antibodies or polyclonal antibodies. In one embodiment, the antibody is a monoclonal antibody that is a
10 chimeric antibody.

An immortal cell line that produces a monoclonal antibody of the present invention is also part of the present invention. In a specific embodiment of this immortal cell line, the monoclonal antibody is prepared against the TACI protein having an amino acid sequence
15 of SEQ ID NO:2 or an antigenic fragment thereof.

The present invention also includes an N-terminal fragment of CAML that is sufficient to bind to the C-terminal 126 amino acid fragment of TACI-1. In one such embodiment, the N-terminal fragment of CAML contains 146 amino acids. This N-terminal fragment of
20 CAML can serve as an inhibitor of TACI-CAML binding.

The present invention includes methods of making TACI proteins, fragments thereof and fusion proteins thereof. In one embodiment the method comprises introducing an expression vector comprising a nucleic acid encoding a polypeptide that is a TACI protein,
25 or a fragment thereof, or a fusion protein thereof, into a host cell and expressing the encoded polypeptide. In a preferred embodiment the expressed polypeptide has a binding affinity for CAML. In a more preferred embodiment the polypeptide, when appropriately stimulated, *in situ*, initiates activation of a transcription factor through the combination of a Ca^{2+} -dependent and a Ca^{2+} -independent pathway. In the most preferred embodiment of
30 this type the expressed polypeptide is a TACI protein having an amino acid sequence of SEQ ID NO:2.

Methods of purifying the expressed polypeptides encoding TACI proteins, fragments thereof and fusion proteins thereof, are also part of the present invention, as are the

purified expressed polypeptides themselves.

The present invention also includes methods for identifying a ligand for a TACI protein.

One embodiment of such a method comprises contacting the N-terminal extracellular

- 5 polypeptide of a TACI protein with a candidate molecule and detecting the binding of the N-terminal extracellular polypeptide with the candidate molecule. The binding of the N-terminal extracellular polypeptide with the candidate molecule indicates that the candidate molecule is ligand.

- 10 In an alternative method for identifying a ligand for a TACI protein, a functional TACI protein is used. In preferred embodiments of this type the functional TACI protein is TACI-1. The binding of the functional TACI protein with the candidate molecule indicates that the candidate molecule is a ligand. In one such embodiment, binding of the candidate molecule to the functional TACI protein is determined by detecting cellular
- 15 activation as a function of the level of activation of the AP-1 pathway. In another embodiment, binding of the candidate molecule to the functional TACI protein is determined by detecting cellular activation as a function of the level of activation of the CAML pathway.

- 20 In another embodiment, binding of the candidate molecule to the functional TACI protein is determined by detecting cellular activation as a function of the level of the concentration of the NF-AT transcription factor. In still another embodiment, binding of the candidate molecule to the functional TACI protein is determined by detecting cellular activation as a function of the level of activation of the NF-KB pathway. In yet another embodiment,
- 25 binding of the candidate molecule to the functional TACI protein is determined by detecting cellular activation as a function of the level of the activation of NF-AT. In this case, the level of activation of NF-AT can be determined by methods including demonstrating cytoplasm to nuclear translocation of NF-AT; the relative dephosphorylation of NF-AT; and/or by NF-AT-dependent transcription.

30

In preferred embodiments, more than one of the above determinations of cellular activation is made, and the candidate molecule is identified as a ligand when all the determinations made indicate the binding of the candidate molecule to the TACI protein. In the most preferred embodiment, all of the above determinations of cellular activation

are made and the candidate molecule is identified as a ligand when all of these determinations indicate that the candidate molecule binds to the TACI protein.

Methods for identifying a ligand for a TACI protein may be performed in a large number of expression systems in the TACI protein can be expressed. One embodiment employs the use of a yeast two-hybrid expression system using the TACI protein as "bait." In another embodiment, interaction cloning from *E. coli* expression-libraries may be employed. In yet another embodiment, functional expression cloning in mammalian cells of the TACI protein can be utilized. In a preferred embodiment, the mammalian cells are B-cell derived lines such as Burkitt's Lymphoma, EBV-immortalized cell lines, or multiple myeloma cell lines. In a more preferred embodiment of this type, the TACI protein is expressed in Jurkat T cells containing a reporter gene under control of an NF-AT promoter. In one such embodiment, the reporter gene encodes secreted alkaline phosphatase (SEAP) as the marker.

15

The present invention also includes methods of screening for an immunosuppressant drug that inhibits the activation of B cells to a greater extent than it inhibits the activation of mature T cells. In preferred embodiments of this type, the immunosuppressant drug inhibits the activation of B cells, but does not inhibit the activation of mature T cells.

Such methods may be performed in transformed T cells, such as a Jurkat T cell, which can be genetically manipulated to express the TACI protein; or in B cells that naturally express the TACI protein. The present invention also includes the immunosuppressant drugs identified which inhibit the activation of B cells, but not the activation of mature T cells.

25

The present invention includes methods of identifying an immunosuppressant drug that selectively blocks the action of B lymphocytes without effecting mature T lymphocytes. One such embodiment comprises contacting a first lymphocyte with a potential drug, wherein the first lymphocyte contains a TACI protein and a first marker protein. The first marker protein is transcribed when the TACI protein is stimulated in the absence of a candidate drug. The TACI protein is stimulated, and the first marker protein is detected under conditions in which if it is transcribed, it is detectable. A potential drug is selected as a candidate drug when the first marker protein cannot be detected. Next, a second lymphocyte is contacted with the candidate drug, wherein the second lymphocyte contains

30

a T cell receptor, and a second marker protein that is transcribed when the T cell receptor is stimulated either in the absence or the presence of the immunosuppressant drug. The T cell receptor is stimulated and the second marker protein is detected under conditions in which if it is transcribed, it is detectable. A candidate drug is identified as an
5 immunosuppressant drug when the second marker protein is detected, since the immunosuppressant drug interferes with the pathway (or aspect thereof) involving the TACI protein but not the pathway (or aspect thereof) involving the T cell receptor.

In one embodiment, the first and second lymphocytes are Jurkat T cells that have been
10 modified to express a TACI protein. In one such particular embodiment the method comprises contacting a first Jurkat T cell with a potential drug, wherein the first Jurkat T cell has been genetically engineered to express a TACI protein and a first reporter gene. The first reporter gene is controlled by an NF-AT promoter, and encodes a first marker protein. The TACI protein is activated, and the amount of expression of the first marker
15 protein is quantified. A potential drug is selected as a candidate drug when the amount of the first marker protein expressed in the presence of the candidate drug is decreased relative to the amount expressed in the absence of the candidate drug. The candidate drug is then contacted with a second Jurkat T cell that contains a T cell receptor and a second reporter gene. The second reporter gene is controlled by an NF-AT promoter, and
20 encodes a second marker protein. The T cell receptor is activated and the amount of expression of the second marker protein is quantified and then compared to the amount of second marker protein expressed in the absence of the candidate drug. A candidate drug is identified as an immunosuppressant drug if either there is no decrease in the amount of expression of the second marker protein in the presence of the candidate drug, or the
25 decrease in the expression of the second marker protein is measurably less than the corresponding decrease in expression of the first marker protein in the presence of the candidate drug.

Any of the marker proteins described herein may be used for this aspect of the invention
30 including SEAP, LacZ or luciferase. The first and second marker protein can be the same protein or two different proteins. The TACI protein may be activated with an antibody raised against a TACI protein, or an active fragment thereof, or a fusion protein thereof. In a preferred embodiment, the TACI protein is TACI-1. Several promoters can be used to control the reporter gene including the NF-AT promoter mentioned above and the AP-1

promoter. Potential drugs can be obtained from any of the drug libraries currently available, and from the chemical and phage libraries described herein.

These and other aspects of the present invention will be better appreciated by reference to
5 the following drawings and Detailed Description.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. The tissue distribution, protein sequence and other salient features of TACI-1.

10 Figure 1 depicts a Northern blot of the tissues indicated probed with TACI-1 cDNA. Other tissues probed include the heart, brain, placenta, lung, liver, skeletal muscle, kidney and the pancreas, none of which showed any TACI-1 mRNA expression.

Figure 2a depicts the amino acid sequence of TACI-1. The proposed transmembrane
15 domain is shown in boxed print and the Prosite TNFR_NGFR motifs are underlined.

Figure 2b depicts a Kyte-Doolittle hydrophobicity plot and schematic diagram of TACI-1 showing the positions of the putative transmembrane domain (solid black) and the TNFR_NGFR motifs (stippled). Figure 2c depicts the cysteine residues of the TACI protein and other TNFR family members.

20 Figure 3. TACI-1 is a cell surface protein. Figure 3a depicts the flow cytometry of TAG Jurkat T cells transiently transfected with a TACI-1 expression plasmid and the transfection marker, pHook (Invitrogen), or the transfection marker pHook alone. Cell surface expression of TACI-1 and the transfection marker protein, HA-Hook, were
25 detected by indirect immunofluorescence using the immunoaffinity-purified anti-TACI-1 polyclonal antibody and the 12CA5 monoclonal antibody. Depicted data represent TACI-1 staining of cells gated for the transfection marker. Figure 3b depicts a photomicrograph showing surface the staining of Cos-7 cells transiently expressing N-terminal FLAG-tagged TACI-1, stained with M2 (anti-FLAG) antibodies and fluorescent anti-mouse IgG
30 antibodies [Bram & Crabtree, *Nature*, 371:355-358 (1994)]. Surface staining was present whether or not cells were permeabilised with detergent.

Figure 4. TACI-1 is a signaling protein that functions in the activation of NF-AT-specific transcription. Figure 4a depicts the activation of an NF-AT-driven secreted alkaline

phosphatase reporter. TAG Jurkat T cells, co-transfected with the SXNFAT reporter [Bram *et al.*, *Mol. Cell. Biol.*, 13:4760-4769 (1993)] and the expression plasmid pBJ5 [Takebe, Y., *et al.*, *Mol. Cell. Biol.*, 8:466-472 (1988)] containing either TACI-1-encoding cDNA (solid triangles) or nothing (circles), were treated with 50 ng/ml PMA and the indicated amounts of ionomycin in the presence (closed symbols) and absence (open symbols) of magnetic beads coated with immunoaffinity-purified anti-TACI-1 polyclonal antibodies. Figure 4b depicts the activation of NF-AT by antibody-cross linked TACI-1 that is blocked by Cyclosporin A (CsA) or FK506. NF-AT activation was determined in TAG Jurkat T cells co-transfected with SXNFAT and pBJ5 (-TACI-1, left) or pBJ5-TACI-1 (+TACI-1, right), and treated with the indicated combinations of PMA (50 ng/ml), ionomycin (2 μ M), CsA (100 ng/ml) and FK506 (500 pg/ml) in the presence of anti-TACI-1 antibody-coated beads ('NS', not stimulated). Figure 4c shows that NF-AT activation by antibody-cross linked TACI-1 requires extracellular calcium. NF-AT activation was measured in the presence of EGTA in Jurkat T cells over expressing TACI-1. The treatments included cross linked anti-TACI-1 (circles), transfection with a C-terminally truncated, calcium-independent calcineurin A subunit (triangles), or activation with the TCR stimulating antibody OKT3 (squares). All cells were co-stimulated by the addition of PMA to 50 ng/ml. Figure 4d depicts the activation of an AP-1-driven secreted alkaline phosphatase reporter. AP-1 activation was measured in TAG Jurkat T cells, co-transfected with a mouse metallothionein AP-1-SEAP reporter [Bram *et al.*, 1991, *supra*] and pBJ5 containing no insert (-TACI-1, left) or TACI-1 cDNA (+TACI-1, right). Cells were incubated in the absence, and with serially increasing amounts, of cross linked anti-TACI-1 antibodies. To control for transfection efficiency, a plasmid containing a constitutive promoter driving the expression of luciferase (EF-Luc) was included.

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Figure 5. TACI-1 interaction with CAML is critical for Ca^{2+} signaling. Figure 5a shows the yeast 2-hybrid interaction. Full-length cDNAs and indicated deletion mutants of TACI-1 and CAML were cloned into the yeast expression plasmids pACT and/or pAS1, and the indicated combinations were tested for interaction with the yeast 2-hybrid system ('+', positive interaction; '-', no interaction; 'ND', not done). Figure 5b depicts the co-immunoprecipitation of CAML with TACI-1. 293T cells were transfected with the indicated combinations of the expression plasmid pBJ5 containing cDNAs for CAML, TACI-1 with an N-terminal FLAG tag, the N-terminal 146 amino acids of CAML (CLX91), or no insert. After incubation for 48 hours, the cells were lysed (1% dodecyl

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maltoside, 20 mM HEPES pH 7.4, 150 mM NaCl, 10% glycerol, 2 mM MgSO₄, 1 mM CaCl₂, 1 mM PMSF) and the lysate was clarified by centrifugation. FLAG-tagged TACI-1 and associated proteins were immunoprecipitated with anti-FLAG monoclonal antibody-conjugated agarose beads and subjected to Western transfer using standard protocols. The Western blot was probed with immunoaffinity-purified anti-CAML polyclonal antibodies followed by chemiluminescent detection (Amersham). Parallel Western blots, performed for each sample, confirmed the expected expression of TACI-1, CAML or the truncated CAML mutant in all transfections. Figure 5c shows that the over expression of the N-terminal half of CAML has a dominant negative effect on TACI-1-induced NF-AT activation. NF-AT activation was determined in TAg Jurkat cells transfected with pBJ5 alone, pBJ5-TACI-1 plus the control plasmid, or pBJ5-TACI-1 with an equivalent amount of CLX91, following treatment with TACI-1-specific antibodies (top). TACI-1 expression in these transfections was determined by Western blot using anti-TACI-1 polyclonal antibodies (bottom). Figure 5d depicts a schematic diagram showing the TACI-1/CAML signal transduction model ('SOC', stores-operated calcium channel).

DETAILED DESCRIPTION OF THE INVENTION

The present invention, in its broadest aspect, provides a novel cell surface receptor that is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes. The role of the cell surface receptor, the Transmembrane Activator and CAML-Interactor (TACI) protein, is to participate in alternate or co-stimulatory pathways to activate or control lymphocyte function. These functions can include response of lymphocytes to foreign antigens in infection, or to cancer, in the graft-rejection, and graft-vs-host reaction. Additionally, activation of lymphocyte signaling plays a key role during lymphocyte development, thus allowing the positive selection of functional lymphocytes and negative selection against self-reactive clones. When activated, the TACI protein stimulates the influx of calcium in lymphocytes. Such calcium influx can, under specific circumstances, lead to the onset of programmed cell death (apoptosis).

The terms "Transmembrane Activator and CAML-Interactor" protein or "TACI" or "TACI protein" are used herein interchangeably with "transmembrane CAML-binding protein" or "TCB" or "TCB protein" and refer to proteinaceous material including single or multiple proteins that act as a novel cell surface receptor that is normally present in

B-lymphocytes. This cell surface receptor has the profile of activities set forth herein. Accordingly, proteins displaying substantially equivalent or altered activity are likewise contemplated. These modifications may be deliberate, for example, such as modifications obtained through site-directed mutagenesis, or may be accidental, such as those obtained
5 through mutations in hosts that are producers of the protein. Included within the scope of these terms are proteins specifically recited herein, as well as all substantially homologous analogs and allelic variations.

In one embodiment the Transmembrane Activator and CAML-Interactor is TACI-1, the
10 human homologue. As shown in the Example, *infra*, TACI-1 initiates a previously undetected signal transduction mechanism that directly links cell surface stimuli to the intracellular signaling molecule, CAML. TACI-1 therefore is a member of a new class of lymphocyte-specific cell surface receptors that modulate the immune response and thus may be used as tool to regulate the immune system in either a positive or a negative
15 direction. In a specific embodiment, TACI-1 has the amino acid sequence set forth in SEQ ID NO:2.

As used herein when a particular nucleic acid is said to encode a protein or polypeptide of the present invention, it is meant that the portion of the particular nucleic acid that consists
20 of the coding sequence for that protein or polypeptide is being identified. For example, the coding region of SEQ ID NO:1 is from nucleotide 14 to nucleotide 895, including the 3 nucleotide translation stop codon at the 3' terminus.

For many purposes, there is a substantial interest in being able to selectively prevent
25 activation of lymphocytes or in the alternative to selectively enhance their activation. For example, for lymphocyte mediated autoimmune diseases, transplant rejection syndrome, and graft-versus host disease, inhibiting the activation of the lymphocyte involved is a viable or necessary treatment for the disease. Furthermore, in the case of myelomas, lymphomas, and leukemias, especially of B cells or immature T cells, there is an interest
30 in slowing the proliferation of cancer cells, which may allow for therapies which are not as destructive to the host as present day therapies. On the other hand, for infections or anti-tumor immune responses, there would be interest in being able to activate lymphocytes to more rapidly respond to the pathogen. Thus, the present invention enables selection of useful agents, *e.g.*, synthetic organic compounds which can activate and/or

deactivate lymphocytes by providing a previously unknown key component in the lymphocyte activation pathway.

In addition, as one understands the activation pathway more completely, one is able to
5 modulate the pathway more effectively, such as providing for agents which are selective
for a particular set or subset of a cellular population. Since in many cases activation
requires co-stimulation, being able to manipulate agents available to the cell may allow for
such cellular activity. In this context, the identification of a target protein that can be
used to develop drugs that modulate a particular pathway, such as the CAML-mediated
10 activation pathway, would allow physicians to particularly treat distinct immune conditions
without over-stimulating or over-suppressing other delicate aspects of the immune system
that are otherwise functioning well. Such targeted stimulation can be used to specifically
amplify the effects of immune stimulators, such as IL-2, thus allowing for the use of
lower doses of the immune stimulator and reducing side effects.

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Furthermore, the invention is an important advance in understanding the CAML-mediated
activation pathway, by permitting selective evaluation and control over the presence or the
absence of a particular intermediate in that pathway. This can be achieved with a knock-
out animal using homologous recombination, integration of genes providing for antisense
20 sequences, introduction of expression constructs involving inducible promoters, and the
like. There is also an interest in being able to determine when a particular gene is being
expressed or is silent, the nature of the cells in which the protein is expressed, and the
like. Therefore, there is substantial interest in identifying specific components of cellular
pathways to allow for understanding an activation pathway, selectively modulating that
25 pathway, and developing drugs which may be active in binding to the target protein. In
this way, drugs can be screened to inhibit such specific pathways.

One particular aspect of the present invention includes a drug screen that uses TACI as a
tool for developing immunosuppressant drugs specific for B-lymphocytes. Such
30 immunosuppressant drugs would selectively block the action of B-lymphocytes, while
leaving T-cells intact to protect patients from viral pathogens. These drugs would be
useful in treating diseases such as Systemic Lupus Erythematosus, a disease due to an
over-activation of the B-lymphocyte response, or multiple myeloma (*e.g.*, Bence-Jones
Myeloma).

Cross-linking the TACI protein activates calcium influx and potentially other secondary messengers. Its mode of action can be mediated by CAML. Unlike known cell surface signaling molecules that are specific for B cells or T cells, such as CD4, CD8, TCR, and CD3, the novel cell surface receptor of the present invention physically interacts with
5 CAML. In addition, there is no sequence homology between the novel cell surface receptor of the present invention and any of these known lymphocyte cell surface signaling molecules, or any other cell surface signaling molecules.

TACI Proteins and Polypeptides

10 In a broad embodiment, the present invention provides TACI proteins. Such proteins include an extracellular domain, a transmembrane domain, and a cytoplasmic domain. The extracellular domain binds ligand. Upon ligand binding, the cytoplasmic domain binds CAML, thus initiating a Ca^{2+} -dependent activation pathway. Receptor oligomerization, *e.g.*, by binding ligand or with an anti-receptor antibody, also initiates a non- Ca^{2+} -dependent
15 activation pathway.

The monomeric form of a TACI protein contains about 295 amino acids. As used herein "about 295 amino acids" means between 265 to 325 amino acids, *i.e.*, roughly *plus or minus* 10%.

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The invention further relates to functionally active polypeptide components of TACI. In one aspect, a functionally active component of TACI is an antigenic fragment, *e.g.*, a peptide reactive with anti-TACI antibodies, or which, when conjugated to a carrier, can be used to generate anti-TACI antibodies. Another functionally active fragment includes the extracellular
25 domain, which binds ligand. The extracellular domain corresponds to the N-terminal fragment of TACI, *e.g.*, from the first amino acid residue of mature TACI to the transmembrane domain. In a specific embodiment, the extracellular domain has the amino acid sequence corresponding to about residue 1 to about residue 166 of SEQ ID NO:6. The ligand-binding region of TACI is a sub-fragment of the N-terminal fragment corresponding
30 to the extracellular domain.

Still another functionally active fragment is the cytoplasmic domain, *e.g.*, from the C-terminal end of the transmembrane domain to the C-terminus of TACI. The cytoplasmic domain of TACI mediates signal transduction via Ca^{2+} -dependent and Ca^{2+} -independent mechanisms.

The cytoplasmic domain includes the CAML-binding region of TACI. In particular, this domain binds a polypeptide corresponding to the N-terminal 146 amino acid residues of CAML. In a specific embodiment, the cytoplasmic domain corresponds to from about amino acid residue 187 to about amino acid residue 293 of SEQ ID NO:2.

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In yet another embodiment, the present invention provides proteolytic fragments of a TACI protein. Such fragments can be prepared by enzymatic digestion, *e.g.*, with Saureus Polypeptides V8 in papain trypsin, chymotrypsin, cathepsin, collagenase, enteropeptidase, thrombin, or fibrinolytic or clotting enzymes; by chemical cleavage, *e.g.*, with cyanogen
10 bromide, or sodium borohydride; etc.

In a specific embodiment, the TACI protein is a receptor protein having the amino acid sequence as shown in SEQ ID NO:2, from residue 1 to residue 293. The present invention contemplates allelic variants of TACI, homologous TACI proteins from other species, and
15 TACI analogs, *e.g.*, prepared by making conservative amino acid substitutions, whether by genetic engineering or by chemical synthesis. A TACI analogue of the invention also includes TACI antigenic fragments that contain, *e.g.*, a terminal cysteine residue to facilitate cross-linking to a carrier protein.

20 There are no reported DNA sequences that are closely related to that for TACI-1. A search for Prosite motifs in TACI-1 reveals one TNFR_NGFR pattern, which consists of C-x(4,6)-[FYH]-x(5,10)-C-x(0,2)-C-x(2,3)-C-x(7,11)-C-x(4,6)-[DNEQSKP]-x(2)-C in the N-terminal half of the protein (where *e.g.*, C-x(4,6)-[FYH] is indicative of an amino acid sequence starting with cysteine followed by either 4, 5, or 6 unspecified amino acids, further followed
25 by either a phenylalanine, a tyrosine, or a histidine). This motif is found in a number of proteins, most of which are receptors for growth factors. Some of these proteins have one copy of this motif. A comparison of the TACI-1 protein sequence with itself reveals a significant repeat between the TNFR_NGFR motif at residues 33-66 and residues 70-104. This analysis drew attention to the presence of two TNFR-type cysteine-rich domains
30 encompassing these regions that indicate that TACI-1 is a member of the superfamily of TNFR receptors.

Synthetic TACI polypeptides. The term "polypeptide" is used in its broadest sense to refer to a compound of two or more subunit amino acids, amino acid analogs, or peptidomimetics.

The subunits may be linked by peptide bonds. In another embodiment, the subunit may be linked by other bonds, *e.g.*, ester, ether, etc. As used herein the term "amino acid" refers to either natural and/or unnatural or synthetic amino acids, including glycine and both the D or L optical isomers, and amino acid analogs and peptidomimetics. A peptide of three or more amino acids is commonly called an oligopeptide if the peptide chain is short. If the peptide chain is long, the peptide is commonly called a polypeptide or a protein. According to the invention, TACI fragments, such as antigenic fragments, or potentially even full-length TACI, can be prepared synthetically.

- 10 Synthetic polypeptides, prepared using the well known techniques of solid phase, liquid phase, or peptide condensation techniques, or any combination thereof, can include natural and unnatural amino acids. Amino acids used for peptide synthesis may be standard Boc (N^{α} -amino protected N^{α} -t-butyloxycarbonyl) amino acid resin with the standard de-protecting; neutralization, coupling and wash protocols of the original solid phase procedure of Merrifield
- 15 [*J. Am. Chem. Soc.*, 85:2149-2154 (1963)], or the base-labile N^{α} -amino protected 9-fluorenylmethoxycarbonyl (Fmoc) amino acids first described by Carpino and Han [*J. Org. Chem.*, 37:3403-3409 (1972)]. Both Fmoc and Boc N^{α} -amino protected amino acids can be obtained from Fluka, Bachem, Advanced Chemtech, Sigma, Cambridge Research Biochemical, Bachem, or Peninsula Labs or other chemical companies familiar to those who
- 20 practice this art. In addition, the method of the invention can be used with other N^{α} -protecting groups that are familiar to those skilled in this art. Solid phase peptide synthesis may be accomplished by techniques familiar to those in the art and provided, for example, in Stewart and Young, 1984, Solid Phase Synthesis, Second Edition, Pierce Chemical Co., Rockford, IL; Fields and Noble, 1990, *Int. J. Pept. Protein Res.* 35:161-214, or using
- 25 automated synthesizers, such as sold by ABS. Thus, polypeptides of the invention may comprise D-amino acids, a combination of D- and L-amino acids, and various "designer" amino acids (*e.g.*, β -methyl amino acids, $C\alpha$ -methyl amino acids, and $N\alpha$ -methyl amino acids, etc.) to convey special properties. Synthetic amino acids include ornithine for lysine, fluorophenylalanine for phenylalanine, and norleucine for leucine or isoleucine. Additionally,
- 30 by assigning specific amino acids at specific coupling steps, α -helices, β turns, β sheets, γ -turns, and cyclic peptides can be generated.

In a further embodiment, subunits of peptides that confer useful chemical and structural properties will be chosen. For example, peptides comprising D-amino acids will be resistant

to L-amino acid-specific proteases *in vivo*. In addition, the present invention envisions preparing peptides that have more well defined structural properties, and the use of peptidomimetics, and peptidomimetic bonds, such as ester bonds, to prepare peptides with novel properties. In another embodiment, a peptide may be generated that incorporates a reduced peptide bond, i.e., $R_1\text{-CH}_2\text{-NH-R}_2$, where R_1 and R_2 are amino acid residues or sequences. A reduced peptide bond may be introduced as a dipeptide subunit. Such a molecule would be resistant to peptide bond hydrolysis, *e.g.*, protease activity. Such peptides would provide ligands with unique function and activity, such as extended half-lives *in vivo* due to resistance to metabolic breakdown, or protease activity. Furthermore, it is well known that in certain systems constrained peptides show enhanced functional activity [Hruby, *Life Sciences*, 31:189-199 (1982)]; [Hruby *et al.*, *Biochem J.*, 268:249-262 (1990)]; the present invention provides a method to produce a constrained peptide that incorporates random sequences at all other positions.

15 *Non-classical amino acids that induce conformational constraints:*

The following non-classical amino acids may be incorporated in the peptide in order to introduce particular conformational motifs: 1,2,3,4-tetrahydroisoquinoline-3-carboxylate [Kazmierski *et al.*, *J. Am. Chem. Soc.*, 113:2275-2283 (1991)]; (2S,3S)-methyl-phenylalanine, (2S,3R)-methyl-phenylalanine, (2R,3S)-methyl-phenylalanine and (2R,3R)-methyl-phenylalanine [Kazmierski and Hruby, *Tetrahedron Lett.*, (1991)]; 2-aminotetrahydronaphthalene-2-carboxylic acid [Landis, *Ph.D. Thesis, University of Arizona*, (1989)]; hydroxy-1,2,3,4-tetrahydroisoquinoline-3-carboxylate [Miyake *et al.*, *J. Takeda Res. Labs.*, 43:53-76 (1989)]; β -carboline (D and L) [Kazmierski, *Ph.D. Thesis, University of Arizona*, (1988)]; HIC (histidine isoquinoline carboxylic acid) [Zechel *et al.*, *Int. J. Pep. Protein Res.*, 43 (1991)]; and HIC (histidine cyclic urea) (Dharanipragada).

The following amino acid analogs and peptidomimetics may be incorporated into a peptide to induce or favor specific secondary structures: LL-Acp (LL-3-amino-2-propenidone-6-carboxylic acid), a β -turn inducing dipeptide analog (Kemp *et al.*, *J. Org. Chem.*, 50:5834-5838 (1985)]; β -sheet inducing analogs [Kemp *et al.*, *Tetrahedron Lett.*, 29:5081-5082 (1988)]; β -turn inducing analogs [Kemp *et al.*, *Tetrahedron Lett.*, 29:5057-5060 (1988)]; α -helix inducing analogs [Kemp *et al.*, *Tetrahedron Lett.*, 29:4935-4938 (1988)]; γ -turn inducing analogs [Kemp *et al.*, *J. Org. Chem.*, 54:109:115 (1989)]; and analogs provided by the following references: Nagai and Sato, *Tetrahedron Lett.*, 26:647-650 (1985); DiMaio *et*

- al.*, *J. Chem. Soc. Perkin Trans.*, p. 1687 (1989); also a Gly-Ala turn analog [Kahn *et al.*, *Tetrahedron Lett.*, **30**:2317 (1989)]; amide bond isostere [Jones *et al.*, *Tetrahedron Lett.*, **29**:3853-3856 (1988)]; tetrazol [Zabrocki *et al.*, *J. Am. Chem. Soc.*, **110**:5875-5880 (1988)]; DTC [Samanen *et al.*, *Int. J. Protein Pep. Res.*, **35**:501:509 (1990)]; and analogs taught in
- 5 Olson *et al.*, *J. Am. Chem. Sci.*, **112**:323-333 (1990) and Garvey *et al.*, *J. Org. Chem.*, **56**:436 (1990). Conformationally restricted mimetics of beta turns and beta bulges, and peptides containing them, are described in U.S. Patent No. 5,440,013, issued August 8, 1995 to Kahn.
- 10 *Protein derivatives.* There are two major classes of peptide-carbohydrate linkages to proteins. First, ether bonds join the serine or threonine hydroxyl to a hydroxyl of the sugar. Second, amide bonds join glutamate or aspartate carboxyl groups to an amino group on the sugar. Acetal and ketal bonds may also bind carbohydrate to peptide.
- 15 Generally, the TACI protein, or a fragment thereof, such as the N-terminal extracellular domain fragment or the C-terminal cytoplasmic CAML-binding domain fragment, may be derivatized by the attachment of one or more chemical moieties to the protein moiety. Chemical modification of biologically active component or components may provide additional advantages under certain circumstances, such as increasing the stability and
- 20 circulation time of the component or components and decreasing immunogenicity. See U.S. Patent No. 4,179,337, Davis *et al.*, issued December 18, 1979. For a review, see Abuchowski *et al.*, in *Enzymes as Drugs* [J.S. Holcberg and J. Roberts, eds. pp. 367-383 (1981)]. A review article describing protein modification and fusion proteins is Francis, *Focus on Growth Factors*, **3**:4-10 (1992), Mediscript: Mountview Court, Friern Barnet Lane,
- 25 London N20, OLD, UK.

The chemical moieties suitable for derivatization may be selected from among water soluble and water insoluble polymers, with water soluble polymers preferred. The polymer selected should preferably be water soluble so that the component to which it is attached does not

30 precipitate in an aqueous environment, such as a physiological environment. Preferably, for therapeutic use of the end-product preparation, the polymer will be pharmaceutically acceptable. One skilled in the art will be able to select the desired polymer based on such considerations as whether the polymer/component conjugate will be used therapeutically, and if so, the desired dosage, circulation time, resistance to proteolysis, and other considerations.

For the present component or components, these may be ascertained using the assays provided herein.

Labeled TACI proteins. The TACI protein of the present invention, and fragments thereof, may be labeled. Suitable labels include enzymes, fluorophores (*e.g.*, fluorescence isothiocyanate (FITC), phycoerythrin (PE), Texas red (TR), rhodamine, free or chelated lanthanide series salts, especially Eu^{3+} , to name a few fluorophores), chromophores, radioisotopes, chelating agents, dyes, colloidal gold, latex particles, ligands (*e.g.*, biotin), and chemiluminescent agents. When a control marker is employed, the same or different labels may be used for the test sample and control marker.

In the instance where a radioactive label, such as the isotopes ^3H , ^{14}C , ^{32}P , ^{35}S , ^{36}Cl , ^{51}Cr , ^{57}Co , ^{58}Co , ^{59}Fe , ^{90}Y , ^{125}I , ^{131}I , and ^{186}Re are used, known currently available counting procedures may be utilized. In the instance where the label is an enzyme, detection may be accomplished by any of the presently utilized calorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques known in the art.

Direct labels are one example of labels which can be used according to the present invention. A direct label has been defined as an entity, which in its natural state, is readily visible, either to the naked eye, or with the aid of an optical filter and/or applied stimulation, *e.g.* U.V. light to promote fluorescence. Among examples of colored labels, which can be used according to the present invention, include metallic sol particles, for example, gold sol particles such as those described by Leuvering (U.S. Patent 4,313,734); dye sol particles such as described by Gribnau et al. (U.S. Patent 4,373,932) and May et al. (WO 88/08534); dyed latex such as described by May, *supra*, Snyder (EP-A 0 280 559 and 0 281 327); or dyes encapsulated in liposomes as described by Campbell et al. (U.S. Patent 4,703,017). Other direct labels include a radio nucleotide, a fluorescent moiety or a luminescent moiety. In addition to these direct labeling devices, indirect labels comprising enzymes can also be used according to the present invention. Various types of enzyme linked immunoassays are well known in the art, for example, alkaline phosphatase and horseradish peroxidase, lysozyme, glucose-6-phosphate dehydrogenase, lactate dehydrogenase, urease, these and others have been discussed in detail by Eva Engvall in Enzyme Immunoassay ELISA and EMIT in *Methods in Enzymology*, 70:419-439 (1980) and in U.S. Patent 4,857,453.

Suitable enzymes include, but are not limited to, alkaline phosphatase and horseradish peroxidase.

Other labels for use in the invention include magnetic beads or magnetic resonance imaging
5 labels.

In another embodiment, a phosphorylation site can be created on an antibody of the invention for labeling with ^{32}P , *e.g.*, as described in European Patent No. 0372707 (application No. 89311108.8) by Pestka, or U.S. Patent No. 5,459,240, issued October 17, 1995 to Foxwell
10 *et al.*

As exemplified herein, proteins, including antibodies, can be labeled by metabolic labeling. Metabolic labeling occurs during *in vitro* incubation of the cells that express the protein in the presence of culture medium supplemented with a metabolic label, such as [^{35}S]-methionine
15 or [^{32}P]-orthophosphate. In addition to metabolic (or biosynthetic) labeling with [^{35}S]-methionine, the invention further contemplates labeling with [^{14}C]-amino acids and [^3H]-amino acids (with the tritium substituted at non-labile positions).

Chimeric TACI Proteins

20 A chimeric TACI protein of the invention may be a protein that is generated by joining a functional domain of a TACI protein, such as the ligand binding domain or the CAML-binding domain, with the complementary domain of another protein, *e.g.*, an alternative receptor. Chimeric constructs can also be prepared with a functionally active fragment of a TACI protein and another functionally active molecule. For example, the
25 extracellular domain of a TACI protein may be joined to the Fc domain of an immunoglobulin. Alternatively, the cytoplasmic domain of a TACI protein could be joined to a receptor ligand, such as transferrin or a hormone, for intracellular targeting. In yet another embodiment, a TACI domain could be joined to another targeting molecule, such as an anti-immunoglobulin heavy chain or light chain molecule (*e.g.*, an Fv portion of an
30 antibody) to specifically target B cells. In still another embodiment, the functionally active fragment of a TACI protein, preferably the N-terminal extracellular domain, can be joined with a glycosylphospholipid, such as glycosylphosphoinositol, anchor signal sequence, preferably located at the C-terminus of the TACI fragment, so that a glycolipid anchored protein is generated [Cross, *Annu. Rev. Cell Biol.*, 6:1-39 (1990); Low, *Biochem. J.*, 244:1-

13 (1987)].

A chimeric TACI receptor can be prepared by joining the extracellular domain of another receptor molecule with a transmembrane domain and the intracellular domain of a TACI protein. In another embodiment, the extracellular domain of TACI can be joined with a transmembrane domain and an intracellular domain of another receptor molecule. The transmembrane domain can be the transmembrane domain of a TACI protein, the transmembrane domain of the other receptor, or a different transmembrane domain. Preferably, the transmembrane domain is from the same protein component of the chimera as the extracellular domain. Chimeric receptors have been described [International Patent Publications WO96/23814; WO96/23881; and WO96/24671]. Chimeric antigen receptors have been described [Capon *et al.*, U.S. Patent No. 5,359,046, issued October 25, 1994], including functional antigen-specific receptors generated in B cells [Sanchez *et al.*, *J. Exp. Med.*, 178:1049-1055 (1993)] and T cells [Burkhardt *et al.*, *Mol. Cell. Biol.*, 14:1095-1103 (1994)] by fusing the Ig α and Ig β signal transduction chains to IgM. Various type I and type II cytokine receptors, including interferon- α , interferon- β , interferon- γ , interleukin-1, interleukin-2, interleukin-3, interleukin-4, interleukin-6, interleukin-8, interleukin-10, interleukin-12, erythropoietin, granulocyte-macrophage colony stimulating factor (CSF), granulocyte-CSF, macrophage-CSF, α -chemokine receptors, and β -chemokine receptors, can provide complementary components in a chimeric receptor comprising a functionally active fragment of a TACI protein.

As those of ordinary skill in the art can appreciate, transmembrane domains are generally functionally equivalent for anchoring a protein in a membrane. However, the presence of specific amino acid residues in a transmembrane domain can affect receptor interaction with, *e.g.*, dimerization, or association with other integral membrane proteins, such as in a multi-protein receptor complex. Thus, selection of a transmembrane domain depends on whether regulatory functions performed by the transmembrane domain are desired or necessary.

30 Nucleic Acids Encoding TACI Proteins

The present invention contemplates isolation of a gene encoding a TACI protein including a full length, or naturally occurring form of TACI protein, and any antigenic fragments thereof from any animal, particularly mammalian and more particularly human, source. As used herein, the term "gene" refers to an assembly of nucleotides that encode a polypeptide, and

includes cDNA and genomic DNA nucleic acids.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, *e.g.*, Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual*, Second Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (herein "Sambrook *et al.*, 1989"); *DNA Cloning: A Practical Approach*, Volumes I and II (D.N. Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed. 1984); *Nucleic Acid Hybridization* [B.D. Hames & S.J. Higgins eds. (1985)]; *Transcription And Translation* [B.D. Hames & S.J. Higgins, eds. (1984)]; *Animal Cell Culture* [R.I. Freshney, ed. (1986)]; *Immobilized Cells And Enzymes* [IRL Press, (1986)]; B. Perbal, *A Practical Guide To Molecular Cloning* (1984); F.M. Ausubel *et al.* (eds.), *Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. (1994).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment. A "replicon" is any genetic element (*e.g.*, plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*, *i.e.*, capable of replication under its own control.

A "cassette" refers to a segment of DNA that can be inserted into a vector at specific restriction sites. The segment of DNA encodes a polypeptide of interest, and the cassette and restriction sites are designed to ensure insertion of the cassette in the proper reading frame for transcription and translation.

A cell has been "transfected" by exogenous or heterologous DNA when such DNA has been introduced inside the cell. A cell has been "transformed" by exogenous or heterologous DNA when the transfected DNA effects a phenotypic change. Preferably, the transforming DNA should be integrated (covalently linked) into chromosomal DNA making up the genome of the cell.

"Heterologous" DNA refers to DNA not naturally located in the cell, or in a chromosomal site of the cell. Preferably, the heterologous DNA includes a gene foreign to the cell.

A "nucleic acid molecule" refers to the phosphate ester polymeric form of ribonucleosides (adenosine, guanosine, uridine or cytidine; "RNA molecules") or deoxyribonucleosides (deoxyadenosine, deoxyguanosine, deoxythymidine, or deoxycytidine; "DNA molecules"), or any phosphoester analogs thereof, such as phosphorothioates and thioesters, in either single
5 stranded form, or a double-stranded helix. Double stranded DNA-DNA, DNA-RNA and RNA-RNA helices are possible. The term nucleic acid molecule, and in particular DNA or RNA molecule, refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear or circular DNA molecules (*e.g.*, restriction fragments), plasmids,
10 and chromosomes. In discussing the structure of particular double-stranded DNA molecules, sequences may be described herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the non-transcribed strand of DNA (*i.e.*, the strand having a sequence homologous to the mRNA). A "recombinant DNA molecule" is a DNA molecule that has undergone a molecular biological manipulation.

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A nucleic acid molecule is "hybridizable" to another nucleic acid molecule, such as a cDNA, genomic DNA, or RNA, when a single stranded form of the nucleic acid molecule can anneal to the other nucleic acid molecule under the appropriate conditions of temperature and solution ionic strength (*see* Sambrook et al., *supra*). The conditions of temperature and ionic
20 strength determine the "stringency" of the hybridization. For preliminary screening for homologous nucleic acids, low stringency hybridization conditions, corresponding to a T_m of 55°, can be used, *e.g.*, 5x SSC, 0.1% SDS, 0.25% milk, and no formamide; or 30% formamide, 5x SSC, 0.5% SDS. Moderate stringency hybridization conditions correspond to a higher T_m , *e.g.*, 40% formamide, with 5x or 6x SCC. High stringency hybridization
25 conditions correspond to the highest T_m , *e.g.*, 50% formamide, 5x or 6x SCC. Hybridization requires that the two nucleic acids contain complementary sequences, although depending on the stringency of the hybridization, mismatches between bases are possible. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementation, variables well known in the art. The greater the degree of
30 similarity or homology between two nucleotide sequences, the greater the value of T_m for hybrids of nucleic acids having those sequences. The relative stability (corresponding to higher T_m) of nucleic acid hybridizations decreases in the following order: RNA:RNA, DNA:RNA, DNA:DNA. For hybrids of greater than 100 nucleotides in length, equations for calculating T_m have been derived (*see* Sambrook et al., *supra*, 9.50-0.51). For

- hybridization with shorter nucleic acids, *i.e.*, oligonucleotides, the position of mismatches becomes more important, and the length of the oligonucleotide determines its specificity (*see* Sambrook et al., *supra*, 11.7-11.8). A minimum length for a hybridizable nucleic acid is at least 10 nucleotides; preferably at least 18 nucleotides; more preferably the length is at least 24 nucleotides and most preferably at least 30 nucleotides in length. In a specific embodiment, a hybridizable nucleic acid of the invention has a sequence corresponding to at least 12 nucleotides, preferably at least 18 nucleotides, more preferably at least 24 nucleotides, and most preferably at least 30 nucleotides in length of SEQ ID NO:1, or more specifically the coding sequence of SEQ ID NO:1.
- In a specific embodiment, the term "standard hybridization conditions" refers to a T_m of 55°C, and utilizes conditions as set forth above. In a preferred embodiment, the T_m is 60°C; in a more preferred embodiment, the T_m is 65°C.
- As used herein, the term "oligonucleotide" refers to a nucleic acid, generally of at least 18 nucleotides, that is hybridizable to a genomic DNA molecule, a cDNA molecule, or an mRNA molecule encoding a TACI protein. Oligonucleotides can be labeled, *e.g.*, with ^{32}P -nucleotides or nucleotides to which a label, such as biotin, has been covalently conjugated (*see* the discussion, *supra*, with respect to labeling TACI polypeptides). In one embodiment, a labeled oligonucleotide can be used as a probe to detect the presence of a nucleic acid encoding a TACI protein. In another embodiment, oligonucleotides (one or both of which may be labeled) can be used as PCR primers, either for cloning full length or a fragment of a TACI protein, or to detect the presence of nucleic acids encoding a TACI protein. In a further embodiment, an oligonucleotide of the invention can form a triple helix with a TACI DNA molecule. Generally, oligonucleotides are prepared synthetically, preferably on a nucleic acid synthesizer. Accordingly, oligonucleotides can be prepared with non-naturally occurring phosphoester analog bonds, such as thioester bonds, etc.
- "Homologous recombination" refers to the insertion of a foreign DNA sequence of a vector in a chromosome. Preferably, the vector targets a specific chromosomal site for homologous recombination. For specific homologous recombination, the vector will contain sufficiently long regions of homology to sequences of the chromosome to allow complementary binding and incorporation of the vector into the chromosome. Longer regions of homology, and greater degrees of sequence similarity, may increase the efficiency of homologous

recombination.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide in a cell *in vitro* or *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include, but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (*e.g.*, mammalian) DNA, and even synthetic DNA sequences. If the coding sequence is intended for expression in a eukaryotic cell, a polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence. In a specific embodiment, a TACI coding sequence of the invention has the nucleotide sequence depicted in SEQ ID NO:1.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, terminators, and the like, that provide for the expression of a coding sequence in a host cell. In eukaryotic cells, polyadenylation signals are control sequences.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site (conveniently defined for example, by mapping with nuclease S1), as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then trans-RNA spliced and translated into the protein encoded by the coding sequence.

A "signal sequence" may be included at the beginning of the coding sequence of a protein to be expressed on the surface of a cell. This sequence encodes a signal peptide, N-terminal to the mature polypeptide, that directs the host cell to translocate the polypeptide. The term "translocation signal sequence" is used herein to refer to this sort of signal sequence.

Translocation signal sequences can be found associated with a variety of proteins native to eukaryotes and prokaryotes, and are often functional in both types of organisms. Interestingly, the TACI of the invention is transported so that the N-terminus is extracellular in the absence of a cleaved signal sequence. Thus, this transmembrane protein is a type III
5 transmembrane protein [see Wilson-Rawls *et al.*, *Virology*, **201**:66-76 (1994)]. Thus, in a construct of the present invention (including a chimeric construct as discussed above), if the N-terminal portion of the construct encodes the N-terminus of TACI, a signal peptide may not be required to obtain expression of the transmembrane TACI protein.

10 As used herein, the term "sequence homology" in all its grammatical forms refers to the relationship between proteins that possess a "common evolutionary origin," including proteins from superfamilies (*e.g.*, the immunoglobulin superfamily) and homologous proteins from different species (*e.g.*, myosin light chain, etc.) [Reeck *et al.*, *Cell*, **50**:667 (1987)]. The present invention naturally contemplates homologues of the human TACI protein as falling
15 within the scope of the invention.

Accordingly, the term "sequence similarity" in all its grammatical forms refers to the degree of identity or correspondence between nucleic acid or amino acid sequences whether or not they share a common evolutionary origin (*see* Reeck *et al.*, *supra*). In common usage, the
20 term "homologous," when modified with an adverb such as "highly," may refer to sequence similarity and not a common evolutionary origin.

In a specific embodiment, two DNA sequences are "substantially homologous" or "substantially similar" when at least about 50% (preferably at least about 75%, and most
25 preferably at least about 90 or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art.
30 See, *e.g.*, Maniatis *et al.*, *supra*; DNA Cloning, Vols. I & II, *supra*; Nucleic Acid Hybridization, *supra*. The present invention contemplates nucleotides that are 50% similar to SEQ ID NO:1 (or its complementary sequence), preferably 60% similar, and more preferably 75% similar. Preferably such substantially similar nucleic acids are homologous.

Similarly, in a particular embodiment, two amino acid sequences are "substantially homologous" or "substantially similar" when greater than 30% of the amino acids are identical, or greater than about 60% are similar (functionally identical). Preferably, the similar or homologous sequences are identified by alignment using, for example, the GCG
5 (Genetics Computer Group, Program Manual for the GCG Package, *Version 7*, Madison, Wisconsin) pileup program.

The term "corresponding to" is used herein to refer similar or homologous sequences, whether the exact position is identical or different from the molecule to which the similarity
10 or homology is measured. Thus, the term "corresponding to" refers to the sequence similarity, and not the numbering of the amino acid residues or nucleotide bases.

A gene encoding a TACI protein, whether genomic DNA or cDNA, can be isolated from any source, particularly from a human cDNA or genomic library. Methods for obtaining TACI
15 protein gene are well known in the art, as described above (*see, e.g., Sambrook et al., 1989, supra*).

Accordingly, any animal cell potentially can serve as the nucleic acid source for the molecular cloning of a *TACI protein* gene. The DNA may be obtained by standard procedures known
20 in the art from cloned DNA (*e.g., a DNA "library"*), and preferably is obtained from a cDNA library prepared from tissues with high level expression of the protein (*e.g., a thymic cDNA library, since peripheral blood cells and in particular lymphocyte cells, appear to have the highest levels of expression of TACI protein*), by chemical synthesis, by CDNA cloning, or by the cloning of genomic DNA, or fragments thereof, purified from the desired cell (See,
25 for example, Sambrook *et al.*, 1989, *supra*; Glover, D.M. (ed.), 1985, *DNA Cloning: A Practical Approach*, MRL Press, Ltd., Oxford, U.K. Vol. I, II). Clones derived from genomic DNA may contain regulatory and intron DNA regions in addition to coding regions; clones derived from cDNA will not contain intron sequences. Whatever the source, the gene should be molecularly cloned into a suitable vector for propagation of the gene.

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In the molecular cloning of the gene from genomic DNA, DNA fragments are generated, some of which will encode the desired gene. The DNA may be cleaved at specific sites using various restriction enzymes. Alternatively, one may use DNase in the presence of manganese to fragment the DNA, or the DNA can be physically sheared, as for example, by

sonication. The linear DNA fragments can then be separated according to size by standard techniques, including but not limited to, agarose and polyacrylamide gel electrophoresis and column chromatography.

- 5 Once the DNA fragments are generated, identification of the specific DNA fragment containing the desired *TACI protein* gene may be accomplished in a number of ways. For example, a portion of a *TACI protein* gene or its specific RNA, or a fragment thereof, can be purified and labeled, the generated DNA fragments may then be screened by nucleic acid hybridization to the labeled probe [Benton and Davis, *Science*, **196**:180 (1977)]; [Grunstein and Hogness, *Proc. Natl. Acad. Sci. U.S.A.*, **72**:3961 (1975)]. For example, a set of oligonucleotides corresponding to the partial amino acid sequence information obtained for the TACI protein can be prepared and used as probes for DNA encoding a TACI protein, or as primers for cDNA or mRNA (*e.g.*, in combination with a poly-T primer for RT-PCR). Preferably, a fragment is selected that is highly unique to the TACI protein of the invention.
- 10 Those DNA fragments with substantial homology to the probe will hybridize. As noted above, the greater the degree of homology, the more stringent hybridization conditions can be used. In a specific embodiment, stringency hybridization conditions are used to identify a homologous *TACI protein* gene.
- 15 Further selection can be carried out on the basis of the properties of the gene, *e.g.*, if the gene encodes a protein product having the isoelectric, electrophoretic, amino acid composition, or partial amino acid sequence of the TACI protein as disclosed herein. Thus, the presence of the gene may be detected by assays based on the physical, chemical, or immunological properties of its expressed product. For example, cDNA clones, or DNA clones which hybrid-select the proper mRNAs, can be selected which produce a protein that, *e.g.*, has similar or identical electrophoretic migration, isoelectric focusing or non-equilibrium pH gel electrophoresis behavior, proteolytic digestion maps, or antigenic properties as known for TACI protein.
- 20 Further selection can be carried out on the basis of the properties of the gene, *e.g.*, if the gene encodes a protein product having the isoelectric, electrophoretic, amino acid composition, or partial amino acid sequence of the TACI protein as disclosed herein. Thus, the presence of the gene may be detected by assays based on the physical, chemical, or immunological properties of its expressed product. For example, cDNA clones, or DNA clones which hybrid-select the proper mRNAs, can be selected which produce a protein that, *e.g.*, has similar or identical electrophoretic migration, isoelectric focusing or non-equilibrium pH gel electrophoresis behavior, proteolytic digestion maps, or antigenic properties as known for TACI protein.
- 25 Further selection can be carried out on the basis of the properties of the gene, *e.g.*, if the gene encodes a protein product having the isoelectric, electrophoretic, amino acid composition, or partial amino acid sequence of the TACI protein as disclosed herein. Thus, the presence of the gene may be detected by assays based on the physical, chemical, or immunological properties of its expressed product. For example, cDNA clones, or DNA clones which hybrid-select the proper mRNAs, can be selected which produce a protein that, *e.g.*, has similar or identical electrophoretic migration, isoelectric focusing or non-equilibrium pH gel electrophoresis behavior, proteolytic digestion maps, or antigenic properties as known for TACI protein.
- 30 A *TACI protein* gene of the invention can also be identified by mRNA selection, *i.e.*, by nucleic acid hybridization followed by *in vitro* translation. In this procedure, nucleotide fragments are used to isolate complementary mRNAs by hybridization. Such DNA fragments may represent available, purified *TACI protein* DNA, or may be synthetic oligonucleotides designed from the partial amino acid sequence information. Immunoprecipitation analysis or

functional assays (*e.g.*, CAML binding activity) of the *in vitro* translation products of the products of the isolated mRNAs identifies the mRNA and, therefore, the complementary DNA fragments, that contain the desired sequences. In addition, specific mRNAs may be selected by adsorption of polysomes isolated from cells to immobilized antibodies specifically
5 directed against TACI protein, such as the rabbit polyclonal anti-human TACI protein antibody described herein.

A radiolabeled *TACI protein* cDNA can be synthesized using the selected mRNA (from the adsorbed polysomes) as a template. The radiolabeled mRNA or cDNA may then be used as
10 a probe to identify homologous *TACI protein* DNA fragments from among other genomic DNA fragments.

The present invention also relates to cloning vectors containing genes encoding analogs and derivatives of the TACI protein of the invention, that have the same or homologous functional
15 activity as TACI protein, and homologs thereof from other species. The production and use of derivatives and analogs related to TACI protein are within the scope of the present invention. In a specific embodiment, the derivative or analog is functionally active, *i.e.*, capable of exhibiting one or more functional activities associated with a full-length, wild-type TACI protein of the invention. In another embodiment, TACI protein containing a different
20 cytoplasmic domain, *e.g.*, one unable to bind CAML but still able to modulate the activation of AP-1. In another aspect, a TACI protein of the invention can be prepared with a lectin domain or domains from another protein, such as the mannose receptor of macrophages or the phospholipase receptor on muscle.

25 TACI protein derivatives can be made by altering encoding nucleic acid sequences by substitutions, additions or deletions that provide for functionally equivalent molecules. Preferably, derivatives are made that have enhanced or increased functional activity relative to native TACI protein. Alternatively, such derivatives may encode soluble fragments of TACI protein extracellular domain that have the same or greater affinity for the natural ligand
30 of TACI protein of the invention. Such soluble derivatives may be potent inhibitors of ligand binding to TACI protein.

Due to the degeneracy of nucleotide coding sequences, other DNA sequences which encode substantially the same amino acid sequence as a *TACI protein* gene may be used in the

practice of the present invention. These include but are not limited to allelic genes, homologous genes from other species, and nucleotide sequences comprising all or portions of *TACI protein* genes which are altered by the substitution of different codons that encode the same amino acid residue within the sequence, thus producing a silent change. Likewise, the TACI protein derivatives of the invention include, but are not limited to, those containing, as a primary amino acid sequence, all or part of the amino acid sequence of a TACI protein including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence resulting in a conservative amino acid substitution. And thus, such a substitution is defined as a conservative substitution.

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For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity, which acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the non-polar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. Amino acids containing aromatic ring structures are phenylalanine, tryptophan, and tyrosine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Such alterations will not be expected to affect apparent molecular weight as determined by polyacrylamide gel electrophoresis, or isoelectric point.

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Particularly preferred substitutions are:

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- Lys for Arg and vice versa such that a positive charge may be maintained;
- Glu for Asp and vice versa such that a negative charge may be maintained;
- Ser for Thr such that a free -OH can be maintained; and
- Gln for Asn such that a free NH₂ can be maintained.

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Amino acid substitutions may also be introduced to substitute an amino acid with a particularly preferable property. For example, a Cys may be introduced at a potential site for disulfide bridges with another Cys. A His may be introduced as a particularly "catalytic" site (*i.e.*, His can act as an acid or base and is the most common amino acid in biochemical catalysis). Pro may be introduced because of its particularly planar structure, which induces

β -turns in the protein's structure.

The genes encoding TACI protein derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can
5 occur at the gene or protein level. For example, the cloned TACI protein gene sequence can be modified by any of numerous strategies known in the art (Sambrook *et al.*, 1989, *supra*). The sequence can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated *in vitro*. In the production
10 of the gene encoding a derivative or analog of TACI protein, care should be taken to ensure that the modified gene remains within the same translational reading frame as the TACI protein gene, uninterrupted by translational stop signals, in the gene region where the desired activity is encoded.

Additionally, the TACI protein-encoding nucleic acid sequence can be mutated *in vitro* or *in vivo*,
15 to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy preexisting ones, to facilitate further *in vitro* modification. Preferably, such mutations enhance the functional activity of the mutated TACI protein gene product. Any technique for mutagenesis known in the art can be used, including but not limited to, *in vitro* site-directed
20 mutagenesis [Hutchinson, C., *et al.*, *J. Biol. Chem.*, **253**:6551 (1978)]; [Zoller and Smith, *DNA*, **3**:479-488 (1984)]; [Oliphant *et al.*, *Gene*, **44**:177 (1986)]; [Hutchinson *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **83**:710 (1986)], use of TAB[®] linkers (Pharmacia), etc. PCR techniques are preferred for site directed mutagenesis (see Higuchi, "Using PCR to Engineer DNA", in *PCR Technology: Principles and Applications for DNA Amplification*, H. Erlich,
25 ed., Stockton Press, Chapter 6, pp. 61-70 (1989)).

The identified and isolated gene can then be inserted into an appropriate cloning vector. A large number of vector-host systems known in the art may be used. Possible vectors include, but are not limited to, plasmids or modified viruses, but the vector system must be compatible
30 with the host cell used. Examples of vectors include, but are not limited to, *E. coli*, bacteriophages such as lambda derivatives, or plasmids such as pBR322 derivatives or pUC plasmid derivatives, *e.g.*, pGEX vectors, pmal-c, pFLAG, etc. The insertion into a cloning vector can, for example, be accomplished by ligating the DNA fragment into a cloning vector which has complementary cohesive termini. However, if the complementary restriction sites

used to fragment the DNA are not present in the cloning vector, the ends of the DNA molecules may be enzymatically modified. Alternatively, any site desired may be produced by ligating nucleotide sequences (linkers) onto the DNA termini; these ligated linkers may comprise specific chemically synthesized oligonucleotides encoding restriction endonuclease
5 recognition sequences. Recombinant molecules can be introduced into host cells via transformation, transfection, infection, electroporation, etc., so that many copies of the gene sequence are generated. Preferably, the cloned gene is contained on a shuttle vector plasmid, which provides for expansion in a cloning cell, *e.g.*, *E. coli*, and facile purification for subsequent insertion into an appropriate expression cell line, if such is desired. For example,
10 a shuttle vector, which is a vector that can replicate in more than one type of organism, can be prepared for replication in both *E. coli* and *Saccharomyces cerevisiae* by linking sequences from an *E. coli* plasmid with sequences from the yeast 2μ plasmid.

In an alternative method, the desired gene may be identified and isolated after insertion into
15 a suitable cloning vector in a "shot gun" approach. Enrichment for the desired gene, for example, by size fractionation, can be done before insertion into the cloning vector.

Expression of Transmembrane Activator and CAML Interactor Polypeptides

The nucleotide sequence coding for the TACI protein, or antigenic fragment, derivative or
20 analog thereof, or a functionally active derivative, including a chimeric protein, thereof, can be inserted into an appropriate expression vector, *i.e.*, a vector which contains the necessary elements for the transcription and translation of the inserted protein-coding sequence. Such elements are termed herein a "promoter." Thus, the nucleic acid encoding the TACI protein of the present invention is operationally associated with a promoter in an expression vector
25 of the invention. Both cDNA and genomic sequences can be cloned and expressed under control of such regulatory sequences. An expression vector also preferably includes a replication origin.

The necessary transcriptional and translational signals can be provided on a recombinant
30 expression vector, or they may be supplied by the native gene encoding a TACI protein and/or its flanking regions.

As pointed out above, potential chimeric partners for TACI protein include those having lectin domains, either from naturally occurring multivalent lectin receptors, such as mannose

receptor of macrophages, natural lectins, or other sources, or a substitute cytoplasmic domain, capable of mediating signal transduction or modifying the endocytic processing.

Potential host-vector systems include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

A recombinant TACI protein of the invention, or functional fragment, derivative, chimeric construct, or analog thereof, may be expressed chromosomally, after integration of the coding sequence by recombination. In this regard, any of a number of amplification systems may be used to achieve high levels of stable gene expression (*See Sambrook et al.*, 1989, *supra*).

The cell containing the recombinant vector comprising the nucleic acid encoding a TACI protein is cultured in an appropriate cell culture medium under conditions that provide for expression of TACI protein by the cell.

Any of the methods previously described for the insertion of DNA fragments into a cloning vector may be used to construct expression vectors containing a gene consisting of appropriate transcriptional/translational control signals and the protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombination (genetic recombination).

Expression of TACI protein may be controlled by any promoter/enhancer element known in the art, but these regulatory elements must be functional in the host selected for expression. Promoters which may be used to control TACI protein gene expression include, but are not limited to, the SV40 early promoter region [Benoist and Chambon, *Nature*, 290:304-310 (1981)], the promoter contained in the 3' long terminal repeat of Rous sarcoma virus [Yamamoto, *et al.*, *Cell*, 22:787-797 (1980)], the herpes thymidine kinase promoter [Wagner *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, 78:1441-1445 (1981)], the regulatory sequences of the metallothionein gene [Brinster *et al.*, *Nature*, 296:39-42 (1982)]; prokaryotic expression

vectors such as the β -lactamase promoter [Villa-Kamaroff, *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **75**:3727-3731 (1978)], or the *tac* promoter [DeBoer, *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **80**:21-25 (1983)]; see also "Useful proteins from recombinant bacteria" in *Scientific American*, **242**:74-94 (1980); promoter elements from yeast or other fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, alkaline phosphatase promoter; and the animal transcriptional control regions, which exhibit tissue specificity and have been utilized in transgenic animals: elastase I gene control region which is active in pancreatic acinar cells [Swift *et al.*, *Cell*, **38**:639-646 (1984)]; [Ornitz *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, **50**:399-409 (1986)]; [MacDonald, *Hepatology*, **7**:425-515 (1987)]; insulin gene control region which is active in pancreatic beta cells [Hanahan, *Nature*, **315**:115-122 (1985)], immunoglobulin gene control region which is active in lymphoid cells [Grosschedl *et al.*, *Cell*, **38**:647-658 (1984)]; [Adames *et al.*, *Nature*, **318**:533-538 (1985)]; [Alexander *et al.*, *Mol. Cell. Biol.*, **7**:1436-1444 (1987)], mouse mammary tumor virus control region which is active in testicular, breast, lymphoid and mast cells [Leder *et al.*, *Cell*, **45**:485-495 (1986)], albumin gene control region which is active in liver [Pinkert *et al.*, *Genes and Devel.*, **1**:268-276 (1987)], alpha-fetoprotein gene control region which is active in liver [Krumlauf *et al.*, *Mol. Cell. Biol.*, **5**:1639-1648 (1985)]; [Hammer *et al.*, *Science*, **235**:53-58 (1987)], alpha 1-antitrypsin gene control region which is active in the liver [Kelsey *et al.*, *Genes and Devel.*, **1**:161-171 (1987)], beta-globin gene control region which is active in myeloid cells [Mogam *et al.*, *Nature*, **315**:338-340 (1985)]; [Kollias *et al.*, *Cell*, **46**:89-94 (1986)], myelin basic protein gene control region which is active in oligodendrocyte cells in the brain [Readhead *et al.*, *Cell*, **48**:703-712 (1987)], myosin light chain-2 gene control region which is active in skeletal muscle [Sani, *Nature*, **314**:283-286 (1985)], and gonadotropic releasing hormone gene control region which is active in the hypothalamus [Mason *et al.*, *Science*, **234**:1372-1378 (1986)].

Expression vectors containing a nucleic acid encoding a TACI protein of the invention can be identified by four general approaches: (a) PCR amplification of the desired plasmid DNA or specific mRNA, (b) nucleic acid hybridization, (c) presence or absence of selection marker gene functions, and (d) expression of inserted sequences. In the first approach, the nucleic acids can be amplified by PCR to provide for detection of the amplified product. In the second approach, the presence of a foreign gene inserted in an expression vector can be detected by nucleic acid hybridization using probes comprising sequences that are homologous to an inserted marker gene. In the third approach, the recombinant vector/host system can

be identified and selected based upon the presence or absence of certain "selection marker" gene functions (*e.g.*, β -galactosidase activity, thymidine kinase activity, resistance to antibiotics, transformation phenotype, occlusion body formation in baculovirus, etc.) caused by the insertion of foreign genes in the vector. In another example, if the nucleic acid encoding a TACI protein is inserted within the "selection marker" gene sequence of the vector, recombinants containing the TACI protein insert can be identified by the absence of the TACI protein gene function. In the fourth approach, recombinant expression vectors can be identified by assaying for the activity, biochemical, or immunological characteristics of the gene product expressed by the recombinant, provided that the expressed protein assumes a functionally active conformation.

A wide variety of host/expression vector combinations may be employed in expressing the DNA sequences of this invention. Useful expression vectors, for example, may consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of SV40 and known bacterial plasmids, *e.g.*, *E. coli* plasmids col E1, pCR1, pBR322, pMal-C2, pET, pGEX [Smith *et al.*, *Gene*, 67:31-40 (1988)], pMB9 and their derivatives, plasmids such as RP4; phage DNAs, *e.g.*, the numerous derivatives of phage λ , *e.g.*, NM989, and other phage DNA, *e.g.*, M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2μ plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

For example, in a baculovirus expression systems, both non-fusion transfer vectors, such as but not limited to pVL941 (*Bam*H1 cloning site; Summers), pVL1393 (*Bam*H1, *Sma*I, *Xba*I, *Eco*R1, *Not*I, *Xma*III, *Bgl*II, and *Pst*I cloning site; Invitrogen), pVL1392 (*Bgl*II, *Pst*I, *Nor*I, *Xma*III, *Eco*RI, *Xba*I, *Sma*I, and *Bam*H1 cloning site; Summers and Invitrogen), and pBlueBacIII (*Bam*H1, *Bgl*II, *Pst*I, *Nco*I, and *Hind*III cloning site, with blue/white recombinant screening possible; Invitrogen), and fusion transfer vectors, such as but not limited to pAc700 (*Bam*H1 and *Kpn*I cloning site, in which the *Bam*H1 recognition site begins with the initiation codon; Summers), pAc701 and pAc702 (same as pAc700, with different reading frames), pAc360 (*Bam*H1 cloning site 36 base pairs downstream of a polyhedrin initiation codon; Invitrogen(195)), and pBlueBacHisA, B, C (three different reading frames, with *Bam*H1, *Bgl*II, *Pst*I, *Nco*I, and *Hind*III cloning site, an N-terminal peptide for ProBond purification,

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C (*Xba*I, *Sph*I, *Sho*I, *Not*I, *Bst*XI, *Eco*RI, *Bam*HI, *Sac*I, *Kpn*I, and *Hind*III cloning site, N-terminal peptide purified with ProBond resin and cleaved with enterokinase; Invitrogen), to mention just two, can be employed according to the invention.

- 5 Once a particular recombinant DNA molecule is identified and isolated, several methods known in the art may be used to propagate it. Once a suitable host system and growth conditions are established, recombinant expression vectors can be propagated and prepared in quantity. As previously explained, the expression vectors which can be used include, but are not limited to, the following vectors or their derivatives: human or animal viruses such
10 as vaccinia virus or adenovirus; insect viruses such as baculovirus; yeast vectors; bacteriophage vectors (*e.g.*, lambda), and plasmid and cosmid DNA vectors, to name but a few.

- In addition, a host cell strain may be chosen which modulates the expression of the inserted
15 sequences, or modifies and processes the gene product in the specific fashion desired. Different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, cleavage *e.g.*, of signal sequence) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example,
20 expression in a bacterial system can be used to produce an non-glycosylated core protein product.

- Vectors are introduced into the desired host cells by methods known in the art, *e.g.*, transfection, electroporation, micro injection, transduction, cell fusion, DEAE dextran,
25 calcium phosphate precipitation, lipofection (lysosome fusion), use of a gene gun, or a DNA vector transporter (see, *e.g.*, Wu *et al.*, *J. Biol. Chem.*, **267**:963-967 (1992); Wu and Wu, *J. Biol. Chem.*, **263**:14621-14624 (1988); Hartmut *et al.*, Canadian Patent Application No. 2,012,311, filed March 15, 1990).

30 Gene Therapy and Transgenic Vectors

A genetic deficiency of a TACI protein can be one of the many factors involved in inherited immunodeficiency. The present invention includes gene therapy with the *TACI protein* cDNA that restores normal lymphocyte function in patients having a genetic defect in the *Transmembrane Activator and CAML Interactor protein* gene. The present invention also

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- 5 Targeted gene delivery is described in International Patent Publication WO 95/28494, published October 1995.

Alternatively, the vector can be introduced *in vivo* by lipofection. For the past decade, there has been increasing use of liposomes for encapsulation and transfection of nucleic acids *in*
10 *vitro*. Synthetic cationic lipids designed to limit the difficulties and dangers encountered with liposome mediated transfection can be used to prepare liposomes for *in vivo* transfection of a gene encoding a marker [Felgner, *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **84**:7413-7417 (1987); see Mackey, *et al.*, *Proc. Natl. Acad. Sci. U.S.A.*, **85**:8027-8031 (1988)]. The use of cationic lipids may promote encapsulation of negatively charged nucleic acids, and also
15 promote fusion with negatively charged cell membranes [Felgner and Ringold, *Science*, **337**:387-388 (1989)]. The use of lipofection to introduce exogenous genes into the specific organs *in vivo* has certain practical advantages. Molecular targeting of liposomes to specific cells represents one area of benefit. It is clear that directing transfection to particular cell types would be particularly advantageous in a tissue with cellular heterogeneity, such as
20 pancreas, liver, kidney, and the brain. Lipids may be chemically coupled to other molecules for the purpose of targeting [see Mackey, *et al.*, *supra*]. Targeted peptides, *e.g.*, hormones or neurotransmitters, and proteins such as antibodies, or non-peptide molecules could be coupled to liposomes chemically.

- 25 It is also possible to introduce the vector *in vivo* as a naked DNA plasmid. Naked DNA vectors for gene therapy can be introduced into the desired host cells by methods known in the art, *e.g.*, transfection, electroporation, micro injection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter [see, *e.g.*, Wu *et al.*, *J. Biol. Chem.*, **267**:963-967 (1992); Wu and Wu, *J. Biol.*
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In a preferred embodiment of the present invention, a gene therapy vector as described above employs a transcription control sequence operably associated with the sequence for the TACI

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In a preferred embodiment of the present invention, a gene therapy vector as described above employs a transcription control sequence operably associated with the sequence for the TACI

- embodiment, *TACI protein* genes can be tested by examining their phenotypic effects when expressed in antisense orientation in wild-type animals. In this approach, expression of the wild-type allele is suppressed, which leads to a mutant phenotype. RNA-RNA duplex formation (antisense-sense) prevents normal handling of mRNA, resulting in partial or complete elimination of wild-type gene effect. This technique has been used to inhibit TK synthesis in tissue culture and to produce phenotypes of the *Kruppel* mutation in *Drosophila*, and the *Shiverer* mutation in mice [Izant *et al.*, *Cell*, **36**:1007-1015 (1984); Green *et al.*, *Annu. Rev. Biochem.*, **55**:569-597 (1986); Katsuki *et al.*, *Science*, **241**:593-595 (1988)]. An important advantage of this approach is that only a small portion of the gene need be expressed for effective inhibition of expression of the entire cognate mRNA. The antisense transgene will be placed under control of its own promoter or another promoter expressed in the correct cell type, and placed upstream of the SV40 polyA site. This transgene will be used to make transgenic mice, or by using gene knockout technology.
- Thus the present invention extends to the preparation of antisense nucleotides and ribozymes that may be used to interfere with the expression of the TACI protein at the translational level. This approach utilizes antisense nucleic acid and ribozymes to block translation of a specific mRNA, either by masking that mRNA with an antisense nucleic acid or cleaving it with a ribozyme. Genes encoding TACI mRNA-specific antisense or ribozyme nucleic acids can be introduced, *e.g.*, using techniques as described above for "Gene Therapy." Alternatively, synthetic antisense or ribozyme oligonucleotides can be prepared.

- Antisense nucleic acids are DNA or RNA molecules that are complementary to at least a portion of a specific mRNA molecule [see Marcus-Sekura, *Anal. Biochem.*, **172**:298 (1988)]. In the cell, they hybridize to that mRNA, forming a double stranded molecule. The cell does not translate an mRNA in this double-stranded form. Therefore, antisense nucleic acids interfere with the expression of mRNA into protein. Oligomers of about fifteen nucleotides and molecules that hybridize to the AUG initiation codon will be particularly efficient, since they are easy to synthesize and are likely to pose fewer problems than larger molecules when introducing them into organ cells. Antisense methods have been used to inhibit the expression of many genes *in vitro* [Marcus-Sekura, 1988, *supra*; Hambor *et al.*, *J. Exp. Med.*, **168**:1237 (1988)]. Preferably synthetic antisense nucleotides contain phosphoester analogs, such as phosphorothiolates, or thioesters, rather than natural phosphoester bonds. Such phosphoester bond analogs are more resistant to degradation, increasing the stability, and therefore the

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contains a signal to terminate transcription prior to the transcription of a region of the allele that encodes TACI protein. In these preferred embodiments it is still more preferred to remove a section of DNA at the beginning of the coding region for the TACI protein and replacing it with the above insertion.

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The present invention also includes a method for producing the knockout mouse of the instant invention that includes: obtaining genomic DNA encoding a TACI protein, constructing a vector containing said genomic DNA and a marker gene wherein said marker gene is placed within the exon of said genomic DNA. The vector is then electroporated into an embryonic stem cell and an embryonic stem cell is selected that has integrated the vector into the genome, wherein the selected cell has integrated the marker gene into the endogenous site of the gene for the TACI protein in the mouse genome. The cell is then injected into a mouse blastocyst which is then re-implanted into a pseudopregnant female mouse, which gives birth to a chimeric mouse containing a defective allele for the TACI protein in its germ line. The chimeric mouse is then mated to a mouse of a standard in-bred line to generate a heterozygous knockout mouse. Two heterozygous mice are then bred generating a homozygous knockout mouse offspring. Detailed protocols for successful gene targeting are well known in the art, and for example as described by Joyner, A. L. (1993) *Gene Targeting: A Practical Approach*. The Practical Approach Series (Rickwood, D., and Hames, B. D., Eds.), IRL Press, Oxford which is hereby incorporated by reference in its entirety.

Another aspect of the invention is a method for selecting a therapeutic agent for possible use as an immunosuppressant which comprises administering a suspected therapeutic agent to the knockout mouse of the present invention and measuring and/or determining the putative therapeutic agent's effect on any of the phenotypic characteristics which may be believed to be related to the immunodeficiency.

A preferred embodiment of this aspect of the invention includes administering a suspected therapeutic agent to the knockout mouse of the present invention and measuring a test response in the knockout mouse, wherein the normal response of the knockout mouse in the absence of a therapeutic agent is characteristically different from that of wild-type mice. The potential therapeutic agents are selected on the basis of whether there is a statistical significance between test response and the normal response. Potential therapeutic agents are selected that show a statistically significant change in the characteristic measured/determined.

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Solid phase support separations are generally performed batch-wise with low-speed centrifugations or by column chromatography. High performance liquid chromatography (HPLC), including such related techniques as FPLC, is presently the most common means of performing liquid chromatography. Size exclusion techniques may also be accomplished
5 with the aid of low speed centrifugation.

In addition size permeation techniques such as gel electrophoretic techniques may be employed. These techniques are generally performed in tubes, slabs or by capillary electrophoresis.

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Almost all steps involving protein purification employ a biological buffer at a pH close to the pKa of that buffer. Typical buffers can be purchased from most biochemical catalogues and include the classical buffers such as Tris, pyrophosphate, monophosphate, and diphosphate, or the Good buffers [Good, N.E., *et al.*, *Biochemistry*, 5:467 (1966)]; [Good, N.E. and
15 Izawa, S., *Meth. Enzymol.*, 24, Part B, 53 (1972)]; and [Ferguson, W.J. and Good, N. E., *Anal. Biochem.*, 104:300 (1980)] such as Mes, Hepes, Mops, tricine and Ches.

Materials to perform all of these techniques are available from a variety of sources such as Sigma Chemical Company in St. Louis, Missouri.

20

Antibodies to the TACI protein

The present invention discloses the protein sequence and properties of a specific Transmembrane Activator and CAML Interactor protein, TACI, thereby enabling the development of antibody reagents specific for the extracellular portion of the receptor.
25 Polyvalent antibody reagents can act to cross-link and activate TACI signaling in lymphocytes, a useful process in situations where enhanced lymphocyte responsiveness is beneficial. Such situations include for example, in the treatment of immunodeficiencies that are either congenital or acquired *e.g.*, AIDS. In addition, these antibody reagents may be used as an adjuvant treatment in cancer in instances that the immune system can aid in the
30 eradication of neoplastic cells. Similarly monovalent antibody reagents can act to block access to TACI in lymphocytes, a process that is useful in situations where depressed lymphocyte responsiveness is beneficial such as during organ transplants.

According to the present invention, the TACI protein produced naturally, recombinantly or

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- [Morrison *et al.*, *J. Bacteriol.*, **159**:870 (1984); Neuberger *et al.*, *Nature*, **312**:604-608 (1984); Takeda *et al.*, *Nature*, **314**:452-454 (1985)] by splicing the genes from a mouse antibody molecule specific for a TACI protein together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention. Such human or humanized chimeric antibodies are preferred for use in therapy of human diseases or disorders (described *infra*), since the human or humanized antibodies are much less likely than xenogeneic antibodies to induce an immune response, in particular an allergic response, themselves.
- 10 According to the invention, techniques described for the production of single chain antibodies [U.S. Patent Nos. 5,476,786 and 5,132,405 to Huston; U.S. Patent 4,946,778] can be adapted to produce the TACI protein-specific single chain antibodies. An additional embodiment of the invention utilizes the techniques described for the construction of Fab expression libraries [Huse *et al.*, *Science*, **246**:1275-1281 (1989)] to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity for a TACI protein, or its derivatives, or analogs.

- Antibody fragments which contain the idiotype of the antibody molecule can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragments which can be generated by reducing the disulfide bridges of the F(ab')₂ fragment, and the Fab fragments which can be generated by treating the antibody molecule with papain and a reducing agent.
- 25 In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, *e.g.*, radioimmunoassay, ELISA (enzyme-linked immunosorbant assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, *in situ* immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary

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TACI protein using various screening assays known in the art.

- Any screening technique known in the art can be used to screen for TACI protein agonists or antagonists. The present invention contemplates screens for small molecule ligands or ligand analogs and mimics, as well as screens for the natural ligand(s) that bind to and agonize or antagonize the TACI protein *in vivo*. For example, natural products libraries can be screened using assays of the invention for molecules that agonize or antagonize the TACI protein activity, or that bind to the extracellular domain or cytoplasmic domain of TACI.
- 10 Knowledge of the primary sequence of the TACI protein, and the similarity of that sequence with proteins of known function, can provide an initial clue as the inhibitors or antagonists of the protein. Identification and screening of antagonists is further facilitated by determining structural features of the protein, *e.g.*, using X-ray crystallography, neutron diffraction, nuclear magnetic resonance spectrometry, and other techniques for structure determination.
- 15 These techniques provide for the rational design or identification of agonists and antagonists.

- Another approach uses recombinant bacteriophage to produce large libraries. Using the "phage method" [Scott and Smith, *Science*, **249**:386-390 (1990); Cwirla, *et al.*, *Proc. Natl. Acad. Sci.*, **87**:6378-6382 (1990); Devlin *et al.*, *Science*, **249**:404-406 (1990)], very large libraries can be constructed (10^6 - 10^8 chemical entities). A second approach uses primarily chemical methods, of which the Geysen method [Geysen *et al.*, *Molecular Immunology*, **23**:709-715 (1986); Geysen *et al.*, *J. Immunologic Method*, **102**:259-274 (1987)] and the method of Fodor *et al.* [*Science*, **251**:767-773 (1991)] are examples. Furka *et al.* [*14th International Congress of Biochemistry, Volume 5*, Abstract FR:013 (1988); Furka, *Int. J. Peptide Protein Res.*, **37**:487-493 (1991)], Houghton [U.S. Patent No. 4,631,211, issued December 1986] and Rutter *et al.* [U.S. Patent No. 5,010,175, issued April 23, 1991] describe methods to produce a mixture of peptides that can be tested as agonists or antagonists.
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- 25
- 30 In another aspect, synthetic libraries [Needels *et al.*, *Proc. Natl. Acad. Sci. USA*, **90**:10700-4 (1993); Ohlmeyer *et al.*, *Proc. Natl. Acad. Sci. USA*, **90**:10922-10926 (1993); Lam *et al.*, International Patent Publication No. WO 92/00252; Kocis *et al.*, International Patent Publication No. WO 9428028, each of which is incorporated herein by reference in its entirety], and the like can be used to screen for the TACI protein ligands according to the

TACI protein using various screening assays known in the art.

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25 December 1986] and Rutter *et al.* [U.S. Patent No. 5,010,175, issued April 23, 1991] describe methods to produce a mixture of peptides that can be tested as agonists or antagonists.

- 30 In another aspect, synthetic libraries [Needels *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:10700-4 (1993); Ohlmeyer *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:10922-10926 (1993); Lam *et al.*, International Patent Publication No. WO 92/00252; Kocis *et al.*, International Patent Publication No. WO 9428028, each of which is incorporated herein by reference in its entirety], and the like can be used to screen for the TACI protein ligands according to the

In a particular embodiment Jurkat T cells are transfected with TACI-1 expression plasmid and a NF-AT-reporter plasmid. Jurkat T cells naturally express the T-cell receptor (TCR). The cells are stimulated by the addition of antibodies to TACI-1, antibodies to TCR, or antibodies to both. Candidate drugs are mixed with the Jurkat T cells and the effect of these drugs is determined. Phage and chemical libraries described above may be used as sources for drug candidates.

These candidate drugs are then applied in a parallel experiment in which antibodies to TCR are used in place of the antibodies to TACI-1. If the candidate drug has no effect on the SEAP signal stimulation due to the antibody-dependent activation of TCR, the candidate drug is identified as having selective inhibition of the TACI-1 activated response. Such selected drugs include that class of drugs which can selectively inhibit the B-cell (antibody producing) response, while allowing T-cell mediated (cellular) immunity to proceed. Such selected drugs may be used to treat the autoimmune diseases described above. Because TACI-1 activates lymphocytes by a novel mechanism (i.e. through direct contact with CAML) it is likely that a significant number of drugs are discoverable that can interfere with the CAML-dependent pathway, yet leave normal signaling through the T-cell receptor intact.

In a preferred embodiment of this type, the NF-AT-reporter plasmid contains the SEAP reporter. This signal is used to measure the degree of inhibition of activation. The SEAP reporter assay can be scaled up so as to be performed by a robot screening apparatus. Drugs that block the activation of TACI-1 but not TCR as measured by the SEAP reporter assay are identified as having selective inhibition of the TACI-1 activated response.

Alternatively, a phage library can be employed. Phage libraries have been constructed which when infected into host *E. coli* produce random peptide sequences of approximately 10 to 15 amino acids [Parmley and Smith, *Gene*, 73:305-318 (1988), Scott and Smith, *Science*, 249:386-249 (1990)]. Specifically, the phage library can be mixed in low dilutions with permissive *E. coli* in low melting point LB agar which is then poured on top of LB agar plates. After incubating the plates at 37°C for a period of time, small clear plaques in a lawn of *E. coli* will form which represents active phage growth and lysis of the *E. coli*. A representative of these phages can be absorbed to nylon filters by placing dry filters onto the agar plates. The filters can be marked for orientation, removed, and placed in washing solutions to block any remaining absorbent sites. The filters can then be placed in a solution

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and antibodies that crosslink the receptor. Ligand agonists or antibody agonists can be administered as described below for treatment of subjects in whom immune stimulation, particularly of B cells, is desired.

- 5 B cell responses can be particularly important in fighting infectious diseases, including, but not limited to, bacterial, viral, protozoan, and parasitic infections. Antibodies against infectious microorganisms can rapidly immobilize the organisms by binding to antigen, followed by complement attack or cell mediated attack. Thus, a TACI agonist of the invention can be provided to a subject who is suffering from an infection to boost humoral
10 immune responses. TACI agonists may be particularly useful for boosting immune responses after vaccination, during challenge with the infectious organism. Thus, subjects particularly at risk for infectious diseases, such as influenza, can supplement a vaccination or memory immunity with a TACI agonist during the flu season. Comparable immune boosting could be used with subjects who are entering or reentering an area with an endemic infectious
15 disease, such as malaria.

- In addition, B cell responses may be important in amplifying immune responses to tumors that express tumor-specific antigens. Thus, a TACI agonist may be provided where endogenous anti-tumor antibodies are detected. Indeed, B cells or plasma cells expressing anti-tumor cell
20 surface immunoglobulin can be selected, such as by panning, and transduced with TACI to allow for an amplification of their antibody production.

- In addition to amplifying beneficial immune responses, the present TACI agonists, *e.g.*, ligands and antibodies, can be used to over-stimulate cells, such as B cells tumors (multiple
25 myelomas, lymphomas, and leukemias), immature T cell tumors (leukemias and thymomas), and autoimmune or inflammatory cells and induce apoptosis in such cells, thereby reducing or eliminating the cancer or autoimmune/inflammatory condition.

- Therapies for boosting cellular immune responses.* Although TACI is found in only a subset
30 of immature T cells, mature T cells can be transfected or transduced *in vivo* or *ex vivo* to express a functional TACI receptor, to amplify cellular immune responses. Preferably, tumor infiltrating cells are selected for such boosting, and reintroduced into the subject to more vigorously fight the tumor.

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In yet another embodiment, the therapeutic compound can be delivered in a controlled release system. For example, an agonist or antagonist to the transmembrane binding protein of the present invention, such as an antibody, may be administered using intravenous infusion, an implantable osmotic pump, a transdermal patch, liposomes, or other modes of administration.

- 5 In one embodiment, a pump may be used [see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.*, **14**:201 (1987); Buchwald *et al.*, *Surgery*, **88**:507 (1980); Saudek *et al.*, *N. Engl. J. Med.*, **321**:574 (1989)]. In another embodiment, polymeric materials can be used [see *Medical Applications of Controlled Release*, Langer and Wise (eds.), CRC Press: Boca Raton, Florida (1974); *Controlled Drug Bioavailability, Drug Product Design and*
- 10 *Performance*, Smolen and Ball (eds.), Wiley: New York (1984); Ranger and Peppas, *J. Macromol. Sci. Rev. Macromol. Chem.*, **23**:61 (1983); see also Levy *et al.*, *Science*, **228**:190 (1985); During *et al.*, *Ann. Neurol.*, **25**:351 (1989); Howard *et al.*, *J. Neurosurg.*, **71**:105 (1989)]. In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, *i.e.*, the brain, thus requiring only a fraction of the systemic dose
- 15 [see, *e.g.*, Goodson, in *Medical Applications of Controlled Release, supra*, vol. 2, pp. 115-138 (1984)]. Preferably, a controlled release device is introduced into a subject in proximity of the site of inappropriate immune activation or a tumor.

Other controlled release systems are discussed in the review by Langer (*Science*, **249**:1527-
20 1533 (1990)).

In a further aspect, recombinant cells that have been transformed with the *TACI protein* gene and that express high levels of the polypeptide can be transplanted in a subject in need of the TACI protein. Preferably autologous cells transformed with TACI protein are transplanted
25 to avoid rejection.

The therapeutic compounds of the present invention can be delivered by intravenous, intraarterial, intraperitoneal, intramuscular, or subcutaneous routes of administration. Alternatively, these compounds, properly formulated, can be administered by nasal or oral
30 administration. A constant supply of these therapeutic compounds can be ensured by providing a therapeutically effective dose (*i.e.*, a dose effective to induce metabolic changes in a subject) at the necessary intervals, *e.g.*, daily, every 12 hours, etc. These parameters will depend on the severity of the disease condition being treated, other actions, such as diet modification, that are implemented, the weight, age, and sex of the subject, and other criteria,

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AP-1 transcription factor, thus providing both signals required for lymphocyte activation. The TACI protein initiates a novel signal transduction mechanism directly linking cell surface stimuli to the intracellular signaling molecule, CAML, and thereby defines a new class of lymphocyte-specific cell surface receptors that modulate the immune response. In addition, the TACI protein is a novel tool that can be used to regulate the immune system in either a positive or a negative direction. TACI-1 is the human homologue of TACI illustrated in the instant example.

Materials And Methods

Molecular cloning and screening. A human B-lymphocyte cDNA library is screened by the two-hybrid system [Fields & Song, *Nature*, 340:245-246 (1989)]; [Durfee *et al.*, *Genes Dev.*, 7:555-569 (1993)], with the full coding region of CAML used as bait. The human CAML cDNA is inserted into the yeast two-hybrid bait vector pAS1. This construct directs the expression of a GAL4-DNA binding domain fused to the entire protein sequence of CAML. A B-lymphocyte library in plasmid pACT is transformed into yeast Y153 and potential interacting plasmids are identified by growth of colonies on media lacking histidine and containing 3-amino triazole.

One clone (TACI-1), out of eight primary positives was identified. The TACI-1 cDNA is subcloned into a mammalian expression plasmid which adds an epitope tag to the amino-terminal end of the expressed protein. This construct is then transfected into the Jurkat T-lymphocyte cell line, COS cells, or NIH3T3 cells. In each case, cell surface expression of the TACI protein is demonstrated. The orientation of the protein is with the N-terminus outside the cell, as the epitope is available for reaction with a specific antibody even without permeablizing the cell membrane. This result facilitated the functional studies described herein.

Secondary screening relied on enforced over expression of positive clones in Jurkat T cells, and assaying for NF-AT activation. (Bram *et al.*, 1993, *supra*) Jurkat T cells transiently transfected with the tagged-TACI-1 construct and an NFAT-reporter plasmid are incubated in medium containing the monoclonal epitope-specific antibody. To maximize cross-linking of TACI-1, the antibodies are bound to beads before addition to the cell suspensions. Following a 24 hour incubation, the activity of the NFAT-reporter is determined. A dramatic induction of NFAT reporter activity is found when cells are

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Results and Discussion

Proteins that can interact with CAML are identified by using a two-hybrid screen (Fields & Song, 1989, *supra*); (Durfee *et al.*, 1993, *supra*) with CAML as bait. To determine whether one of these identified CAML-binding proteins can affect Ca^{2+} signaling in T-cells, their ability to modulate the activity of the Ca^{2+} -dependent transcription factor NF-AT is examined [Truneh *et al.*, *Nature*, **313**:318-321 (1985)]; [Verweij *et al.*, *J. Biol. Chem.*, **265**:15788-15795 (1990)]; [Karttunen & Shastri, *Proc. Natl. Acad. Sci. USA*, **88**:3972-3976 (1991)]; [Emmel *et al.*, *Science*, **246**:1617-1620 (1989)]. Enforced over expression of the two-hybrid clones in Jurkat T-cells reveals that one clone (encoding the TACI-1 protein), replaced the requirement for Ca^{2+} influx, implying that TACI-1 lies in the same signal pathway as CAML. Northern blot analysis for TACI-1 mRNA demonstrates a 1.4 kb mRNA expressed only in spleen, small intestine, thymus and peripheral blood lymphocytes suggesting a limited expression of TACI-1 (Figure 1). The pattern observed is consistent with the expression of TACI-1 being predominantly in peripheral blood cells, since peripheral blood cells, and in particular lymphocytes, can be present in all of these organs (including the Peyer's patches lining the small intestine.) Furthermore, there is no detection of expression in colon, testis, ovary, or prostate. In addition, the TACI-1 protein is detected in all normal peripheral B lymphocytes using specific-antibody staining. There is no detectable protein expressed in peripheral T-lymphocytes, monocytes or neutrophils.

Determination of the DNA sequence from both strands of the DNA isolated reveals a complete open reading frame of 1325 base pairs, which is predicted to encode a protein of 293 amino acids. The deduced amino acid sequence of TACI-1 (Figure 2a) includes a single hydrophobic region (residues 167 to 186) that has features of a membrane spanning segment (Figure 2b). Analysis of the protein sequence by the method of Sipos [Sipos & von Heijne, *Eur. J. Biochem.*, **213**:1333-1340 (1993)]; [Claros & von Heijne, *Comput. Appl. Biosci.*, **10**:685-686 (1994)], predicts extracellular exposure for the N-terminus and cytoplasmic exposure for the C-terminus. Although TACI-1 lacks an N-terminal signal sequence, the presence of an upstream stop codon indicates that the complete open reading frame is contained within the clone. TACI-1 is relatively rich in cysteine residues, but there is no significant sequence similarity or homology to any other disclosed protein. A search for Prosite motifs in TACI-1 reveals one TNFR_NGFR motif [Bairoch, *Nucleic Acids Res.*, **21**:3097-3103 (1993)] (residues 33-71) N-terminal to a putative transmembrane

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- 15 Activation of NF-AT by CAML requires exogenous stimulation of protein kinase C by the addition of phorbol ester (Bram & Crabtree, 1994, *supra*). Antibody-cross linked TACI-1, however, is able to activate NF-AT in the absence of either PMA or ionomycin (Figure 4b, solid bars). Experiments examining the activation of an AP-1 reporter by the over expression of TACI-1 shows that AP-1 activation is elevated (over four-fold) in TACI-1-
20 transfected Jurkat T cells. This effect can be further enhanced with the addition of cross-linked anti-TACI-1 antibodies (Figure 4d). Therefore, TACI-1 initiates Ca^{2+} influx, which in turns activates calcineurin, as well as activates the AP-1 pathway following stimulation, thereby mediating the fulfillment of both requirements for the activation of NF-AT.
- 25 Further confirmation that TACI-1 interacts with CAML can be demonstrated by their specific interaction in a two-hybrid reverse swap experiment (Durfee *et al.*, 1993, *supra*) (Figure 5a). To define the critical amino acid residues involved in the interaction, deletion mutants of both TACI-1 and CAML are tested for their ability to physically
30 associate (Figure 5a). The C-terminal 126 amino acids of TACI-1 are found to be sufficient for binding to the N-terminal 146 amino acids of CAML. Additional evidence for the *in vivo* association of TACI-1 with CAML is provided by experiments in which full length CAML and a mutant comprising the 146 N-terminal amino acid residues of CAML are co-immunoprecipitated with TACI-1 from cell lysates (Figure 5b). Therefore,

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CD3 T-cell receptor, CD2, CD20, and Thy-1. These proteins have no sequence-homology with TACI-1, and it is likely that they play different roles from each other, either in terms of response to different extracellular signals, and/or in terms of developmental stage of expression on lymphocytes. TACI-1 must also play a role in the modulation of the function of lymphocytes in alternate and/or co-stimulatory pathways. Thus, in addition to defining a new signaling mechanism, TACI-1 is a novel lymphocyte-specific receptor capable of activating T-cells.

The following is a list of documents related to the above disclosure and particularly to the experimental procedures and discussions. These documents, and all others cited above, should be considered as incorporated by reference in their entirety.

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14. Fiering, S., *et al.*, *Genes Dev.*, **4**:1823-34 (1990).
15. Bram, R.J., Hung, D.T., Martin, P.K., Schreiber, S.L. & Crabtree, G.R., *Mol.*
- 30 *Cell. Biol.*, **13**:4760-9 (1993).
16. Friedman, J. & Weissman, I., *Cell*, **66**:799-806 (1991).
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18. Hubbard, M.J. & Klee, C.B., *Biochemistry*, **28**:1868-74 (1989).
19. O'Keefe, S.J., Tamura, J., Kincaid, R.L., Tocci, M.J. & O'Neill, E.A., *Nature*,

CD3 T-cell receptor, CD2, CD20, and Thy-1. These proteins have no sequence-homology with TACI-1, and it is likely that they play different roles from each other, either in terms of response to different extracellular signals, and/or in terms of developmental stage of expression on lymphocytes. TACI-1 must also play a role in the modulation of the function of lymphocytes in alternate and/or co-stimulatory pathways. Thus, in addition to defining a new signaling mechanism, TACI-1 is a novel lymphocyte-specific receptor capable of activating T-cells.

The following is a list of documents related to the above disclosure and particularly to the experimental procedures and discussions. These documents, and all others cited above, should be considered as incorporated by reference in their entirety.

1. Imboden, J.B., Weiss, A. & Stobo, J.D., *J. Immunol.*, **134**:663-5 (1985).
2. Crabtree, G.R. & Clipstone, N.A., *Annu. Rev. Biochem.*, **63**:1045-83 (1994).
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9. Karttunen, J. & Shastri, N., *Proc. Natl. Acad. Sci. USA*, **88**:3972-6 (1991).
10. Sipos, L. & von Heijne, G., *Eur. J. Biochem.*, **213**:1333-40 (1993).
- 25 11. Claros, M.G. & von Heijne, G. *Comput. Appl. Biosci.*, **10**:685-6 (1994).
12. Bairoch, A., *Nucleic Acids Res.*, **21**:3097-103 (1993).
13. Wilson-Rawls, J., Deutscher, S.L. & Wold, W.S., *Virology*, **201**:66-76 (1994).
14. Fiering, S., *et al.*, *Genes Dev.*, **4**:1823-34 (1990).
15. Bram, R.J., Hung, D.T., Martin, P.K., Schreiber, S.L. & Crabtree, G.R., *Mol.*
- 30 *Cell. Biol.*, **13**:4760-9 (1993).
16. Friedman, J. & Weissman, I., *Cell*, **66**:799-806 (1991).
17. Liu, J., *et al.*, *Cell*, **66**:807-15 (1991).
18. Hubbard, M.J. & Klee, C.B., *Biochemistry*, **28**:1868-74 (1989).
19. O'Keefe, S.J., Tamura, J., Kincaid, R.L., Tocci, M.J. & O'Neill, E.A., *Nature*,

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bram, Richard J.
von Bulow, Gotz
- (ii) TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
 - (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
 - (C) CITY: Hackensack
 - (D) STATE: New Jersey
 - (E) COUNTRY: USA
 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 28-FEB-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 1340-1-007
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCATCCTGA GTAATGAGTG GCCTGGGCCG GAGCAGGCCG GGTGGCCGGA GCCGTGTGGA	60
CCAGGAGGAG CGCTTTCCAC AGGGCCTGTG GACGGGGGTG GCTATGAGAT CTTGCCCCGA	120
AGAGCAGTAC TGGGATCCTC TGCTGGGTAC CTGCATGTCC TGCAAAACCA TTTGCAACCA	180
TCAGAGCCAG CGCACCTGTG CAGCCTTCTG CAGGTCATC AGCTGCCGCA AGGAGCAAGG	240
CAAGTTCTAT GACCATCTCC TGAGGGACTG CATCAGCTGT GCCTCCATCT GTGGACAGCA	300
CCCTAAGCAA TGTGCATACT TCTGTGAGAA CAAGCTCAGG AGCCCAGTGA ACCTTCCACC	360

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bram, Richard J.
von Bulow, Gotz
- (ii) TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: David A. Jackson, Esq.
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Floor
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 - (F) ZIP: 07601
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 28-FEB-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Jackson Esq., David A.
 - (B) REGISTRATION NUMBER: 26,742
 - (C) REFERENCE/DOCKET NUMBER: 1340-1-007
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 201-487-5800
 - (B) TELEFAX: 201-343-1684

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCATCCTGA GTAATGAGTG GCCTGGGCCG GAGCAGGCCA GGTGGCCGGA GCCGTGTGGA	60
CCAGGAGGAG CGCTTTCCAC AGGGCCTGTG GACGGGGGTG GCTATGAGAT CCTGCCCCGA	120
AGAGCAGTAC TGGGATCCTC TGCTGGGTAC CTGCATGTCC TGCAAACCA TTTGCAACCA	180
TCAGAGCCAG CGCACCTGTG CAGCCTTCTG CAGGTCACTC AGCTGCCGCA AGGAGCAAGG	240
CAAGTTCTAT GACCATCTCC TGAGGGACTG CATCAGCTGT GCCTCCATCT GTGGACAGCA	300
CCCTAAGCAA TGTGCATACT TCTGTGAGAA CAAGCTCAGG AGCCCAGTGA ACCTTCCACC	360

100	105	110
Asn Leu Pro Pro Glu Leu Arg Arg	Gln Arg Ser Gly Glu Val Glu Asn	
115	120	125
Asn Ser Asp Asn Ser Gly Arg Tyr	Gln Gly Leu Glu His Arg Gly Ser	
130	135	140
Glu Ala Ser Pro Ala Leu Pro Gly	Leu Lys Leu Ser Ala Asp Gln Val	
145	150	155
Ala Leu Val Tyr Ser Thr Leu Gly	Leu Cys Leu Cys Ala Val Leu Cys	
165	170	175
Cys Phe Leu Val Ala Val Ala Cys	Phe Leu Lys Lys Arg Gly Asp Pro	
180	185	190
Cys Ser Cys Gln Pro Arg Ser Arg	Pro Arg Gln Ser Pro Ala Lys Ser	
195	200	205
Ser Gln Asp His Ala Met Glu Ala	Gly Ser Pro Val Ser Thr Ser Pro	
210	215	220
Glu Pro Val Glu Thr Cys Ser Phe	Cys Phe Pro Glu Cys Arg Ala Pro	
225	230	235
Thr Gln Glu Ser Ala Val Thr Pro	Gly Thr Pro Asp Pro Thr Cys Ala	
245	250	255
Gly Arg Trp Gly Cys His Thr Arg	Thr Thr Val Leu Gln Pro Cys Pro	
260	265	270
His Ile Pro Asp Ser Gly Leu Gly	Ile Val Cys Val Pro Ala Gln Glu	
275	280	285
Gly Gly Pro Gly Ala		
290		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGAAGAGGG GGGATCCCTG CTCCTGCCAG CCCCCTCAA GGCCCCGTCA AAGTCCGGCC	60
AAGTCTTCCC AGGATCACGC GATGGAAGCC GGCAGCCCTG TGAGCACATC CCCCAGCCA	120
GTGGAGACCT GCAGCTTCTG CTTCCCTGAG TGCAGGGCGC CCACGCAGGA GAGCGCAGTC	180
ACGCCTGGGA CCCCCGACCC CACTTGTGCT GGAAGGTGGG GGTGCCACAC CAGGACCACA	240
GTCTCTGAGC CTTGCCCACA CATCCCAGAC AGTGGCCTTG GCATTGTGTG TGTGCCTGCC	300
CAGGAGGGGG GCCCAGGTGC A	321

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid

71

100	105	110
Asn Leu Pro Pro Glu Leu Arg	Arg Gln Arg Ser Gly Glu Val Glu Asn	
115	120	125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser		
130	135	140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val		
145	150	155
Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys		
165	170	175
Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro		
180	185	190
Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser		
195	200	205
Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro		
210	215	220
Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro		
225	230	235
Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala		
245	250	255
Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro		
260	265	270
His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu		
275	280	285
Gly Gly Pro Gly Ala		
290		

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGAAGAGGG GGGATCCCTG CTCCTGCCAG CCCCCTCAA GGCCCCGTCA AAGTCCGGCC	60
AAGTCTTCCC AGGATCACGC GATGGAAGCC GGCAGCCCTG TGAGCACATC CCCCAGCCA	120
GTGGAGACCT GCAGTTCTG CTTCCTGAG TGCAGGGCGC CCACGCAGGA GAGCGCAGTC	180
ACGCCTGGGA CCCCCGACCC CACTTGTGCT GGAAGGTGGG GGTGCCACAC CAGGACCACA	240
GTCTGCGAGC CTTGCCCCA CATCCAGAC AGTGGCCTTG GCATTGTGTG TGTGCCTGCC	300
CAGGAGGGGG GCCCAGGTGC A	321

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: N-terminal

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1           5           10           15
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20           25           30
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35           40           45
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50           55           60
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65           70           75           80
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85           90           95
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
 100          105          110
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
 115          120          125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
 130          135          140
Glu/Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
 145          150          155          160
Ala Leu Val Tyr Ser Thr
 165

```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGGGCTCT GCCTGTGTGC CGTCCTCTGC TGCTTCCTGG TGGCGGTGGC CTGCTTCCTC

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (iii) HYPOTHETICAL: NO

- (v) FRAGMENT TYPE: N-terminal

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp
 1           5           10          15
Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg
 20          25          30
Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
 35          40          45
Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
 50          55          60
Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp
 65          70          75          80
His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
 85          90          95
Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
100         105         110
Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
115         120         125
Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
130         135         140
Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
145         150         155         160
Ala Leu Val Tyr Ser Thr
165

```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGGGCTCT GCCTGTGTGC CGTCTCTGCG TGCTTCCTGG TGGCGGTGGC CTGCTTCCTC

WHAT IS CLAIMED IS:

- 1 1. An isolated nucleic acid encoding a Transmembrane Activator and
2 CAML-Interactor (TACI) protein, wherein said nucleic acid has a nucleotide sequence
3 having at least 60% similarity with the coding sequence of SEQ ID NO:1.
- 1 2. The isolated nucleic acid of Claim 1, wherein the nucleotide sequence consists of
2 the coding sequence of SEQ ID NO:1.
- 1 3. An isolated nucleic acid consisting of at least 18 nucleotides, wherein said nucleic
2 acid hybridizes to SEQ ID NO:1 under standard hybridization procedures.
- 1 4. An isolated nucleic acid consisting of at least 18 nucleotides of a nucleotide
2 sequence that encodes a Transmembrane Activator and CAML-Interactor (TACI) protein,
3 wherein said TACI protein has an amino acid sequence selected from the group consisting
4 of SEQ ID NO:2, and SEQ ID NO:2 comprising a conservative substitution thereof.
- 1 5. The isolated nucleic acid of Claim 4 that encodes a C-terminal fragment of the
2 TACI protein that is sufficient to bind to the N-terminal 146 amino acids of CAML.
- 1 6. The isolated nucleic acid of Claim 5, wherein the C-terminal fragment of the
2 TACI protein has an amino acid sequence selected from the group consisting of SEQ ID
3 NO:4, and SEQ ID NO:4 comprising a conservative substitution thereof.
- 1 7. The isolated nucleic acid of Claim 4 that encodes an N-terminal fragment of the
2 TACI protein corresponding to the regulatory extracellular domain.
- 1 8. The isolated nucleic acid of Claim 7, wherein the N-terminal fragment of the
2 TACI protein has an amino acid sequence selected from the group consisting of SEQ ID
3 NO:6, and SEQ ID NO:6 comprising a conservative substitution thereof.
- 1 9. The isolated nucleic acid of Claim 4 that encodes said TACI protein.
- 1 10. A DNA construct comprising the isolated nucleic acid of Claim 4, wherein the

WHAT IS CLAIMED IS:

- 1 1. An isolated nucleic acid encoding a Transmembrane Activator and
2 CAML-Interactor (TACI) protein, wherein said nucleic acid has a nucleotide sequence
3 having at least 60% similarity with the coding sequence of SEQ ID NO:1.
- 1 2. The isolated nucleic acid of Claim 1, wherein the nucleotide sequence consists of
2 the coding sequence of SEQ ID NO:1.
- 1 3. An isolated nucleic acid consisting of at least 18 nucleotides, wherein said nucleic
2 acid hybridizes to SEQ ID NO:1 under standard hybridization procedures.
- 1 4. An isolated nucleic acid consisting of at least 18 nucleotides of a nucleotide
2 sequence that encodes a Transmembrane Activator and CAML-Interactor (TACI) protein,
3 wherein said TACI protein has an amino acid sequence selected from the group consisting
4 of SEQ ID NO:2, and SEQ ID NO:2 comprising a conservative substitution thereof.
- 1 5. The isolated nucleic acid of Claim 4 that encodes a C-terminal fragment of the
2 TACI protein that is sufficient to bind to the N-terminal 146 amino acids of CAML.
- 1 6. The isolated nucleic acid of Claim 5, wherein the C-terminal fragment of the
2 TACI protein has an amino acid sequence selected from the group consisting of SEQ ID
3 NO:4, and SEQ ID NO:4 comprising a conservative substitution thereof.
- 1 7. The isolated nucleic acid of Claim 4 that encodes an N-terminal fragment of the
2 TACI protein corresponding to the regulatory extracellular domain.
- 1 8. The isolated nucleic acid of Claim 7, wherein the N-terminal fragment of the
2 TACI protein has an amino acid sequence selected from the group consisting of SEQ ID
3 NO:6, and SEQ ID NO:6 comprising a conservative substitution thereof.
- 1 9. The isolated nucleic acid of Claim 4 that encodes said TACI protein.
- 1 10. A DNA construct comprising the isolated nucleic acid of Claim 4, wherein the

3 membrane spanning segment, and a cytoplasmic domain that has a binding affinity for
4 CAML, wherein said TACI protein is a plasma membrane receptor that interacts directly
5 with an intracellular organelle in lymphocytes.

1 22. The isolated TACI protein of Claim 21 which further comprises the following
2 characteristics:

- 3 (a) the monomer consists of about 295 amino acids;
4 (b) it contains two TNFR motifs; and
5 (b) when appropriately stimulated, *in situ*, it initiates activation of a
6 transcription factor through the combination of a Ca^{2+} -dependent and a Ca^{2+} -independent
7 pathway.

1 23. An antisense nucleic acid that hybridizes under physiological conditions to an
2 mRNA encoding the TACI protein of Claim 20.

1 24. A knockout mouse comprising a first and second allele, wherein
2 (a) said first allele and said second allele each naturally encode and express
3 the functional TACI protein of Claim 20;
4 (b) said first allele contains a defect; and
5 (c) said defect prevents the first allele from expressing a functional TACI
6 protein.

1 25. The knockout mouse of Claim 24 wherein
2 (a) said second allele also contains said defect; and
3 (b) said defect prevents said second allele from expressing a functional TACI
4 protein, whereby the knockout mouse does not express a functional TACI protein.

1 26. An antibody to the polypeptide of Claim 15.

1 27. The antibody of Claim 26 that is a monoclonal antibody.

1 28. An immortal cell line that produces a monoclonal antibody according to Claim 27.

1 29. A method of making a polypeptide of Claim 15 by introducing an expression

3 membrane spanning segment, and a cytoplasmic domain that has a binding affinity for
4 CAML, wherein said TACI protein is a plasma membrane receptor that interacts directly
5 with an intracellular organelle in lymphocytes.

1 22. The isolated TACI protein of Claim 21 which further comprises the following
2 characteristics:

- 3 (a) the monomer consists of about 295 amino acids;
- 4 (b) it contains two TNFR motifs; and
- 5 (b) when appropriately stimulated, *in situ*, it initiates activation of a
6 transcription factor through the combination of a Ca^{2+} -dependent and a Ca^{2+} -independent
7 pathway.

1 23. An antisense nucleic acid that hybridizes under physiological conditions to an
2 mRNA encoding the TACI protein of Claim 20.

1 24. A knockout mouse comprising a first and second allele, wherein
2 (a) said first allele and said second allele each naturally encode and express
3 the functional TACI protein of Claim 20;
4 (b) said first allele contains a defect; and
5 (c) said defect prevents the first allele from expressing a functional TACI
6 protein.

1 25. The knockout mouse of Claim 24 wherein
2 (a) said second allele also contains said defect; and
3 (b) said defect prevents said second allele from expressing a functional TACI
4 protein, whereby the knockout mouse does not express a functional TACI protein.

1 26. An antibody to the polypeptide of Claim 15.

1 27. The antibody of Claim 26 that is a monoclonal antibody.

1 28. An immortal cell line that produces a monoclonal antibody according to Claim 27.

1 29. A method of making a polypeptide of Claim 15 by introducing an expression

1 36. The method according to Claim 34, wherein the TACI protein is expressed in
2 Jurkat cells containing a reporter gene under control of an NF-AT promoter.

1 37. The method of Claim 36, wherein the reporter gene encodes a marker that is
2 secreted alkaline phosphatase (SEAP).

1 38. A method of identifying an immunosuppressant drug that selectively blocks the
2 action of B lymphocytes without effecting mature T lymphocytes comprising
3 (a) contacting a first lymphocyte with a potential drug; wherein the first
4 lymphocyte contains TACI, and a first marker protein, and wherein said first marker
5 protein is transcribed when TACI is stimulated in the absence of a candidate drug;
6 (b) stimulating TACI;
7 (c) detecting the first marker protein under conditions in which the transcribed
8 first marker protein is detectable; wherein a potential drug is selected as a candidate drug
9 when the first marker protein cannot be detected;
10 (d) contacting a second lymphocyte with the candidate drug; wherein the
11 second lymphocyte contains a T cell receptor and a second marker protein, and wherein
12 said second marker protein is transcribed when the T cell receptor is stimulated either in
13 the absence or the presence of an immunosuppressant drug;
14 (e) stimulating the T cell receptor;
15 (g) detecting the second marker protein under conditions in which the
16 transcribed second marker protein is detectable; wherein a candidate drug is identified as
17 an immunosuppressant drug when the second marker protein is detected.

1 39. The method of Claim 38 wherein stimulating TACI is performed with an antibody
2 raised against a TACI protein.

1 36. The method according to Claim 34, wherein the TACI protein is expressed in
2 Jurkat cells containing a reporter gene under control of an NF-AT promoter.

1 37. The method of Claim 36, wherein the reporter gene encodes a marker that is
2 secreted alkaline phosphatase (SEAP).

1 38. A method of identifying an immunosuppressant drug that selectively blocks the
2 action of B lymphocytes without effecting mature T lymphocytes comprising

3 (a) contacting a first lymphocyte with a potential drug; wherein the first
4 lymphocyte contains TACI, and a first marker protein, and wherein said first marker
5 protein is transcribed when TACI is stimulated in the absence of a candidate drug;

6 (b) stimulating TACI;

7 (c) detecting the first marker protein under conditions in which the transcribed
8 first marker protein is detectable; wherein a potential drug is selected as a candidate drug
9 when the first marker protein cannot be detected;

10 (d) contacting a second lymphocyte with the candidate drug; wherein the
11 second lymphocyte contains a T cell receptor and a second marker protein, and wherein
12 said second marker protein is transcribed when the T cell receptor is stimulated either in
13 the absence or the presence of an immunosuppressant drug;

14 (e) stimulating the T cell receptor;

15 (g) detecting the second marker protein under conditions in which the
16 transcribed second marker protein is detectable; wherein a candidate drug is identified as
17 an immunosuppressant drug when the second marker protein is detected.

1 39. The method of Claim 38 wherein stimulating TACI is performed with an antibody
2 raised against a TACI protein.

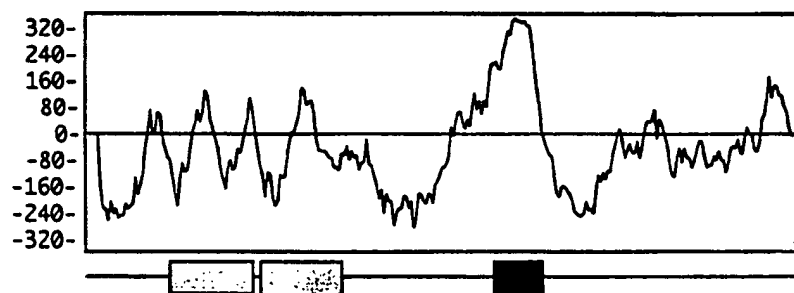
2/5

a.

MSGLGRSRAGGRSRVDQEERFPQGLWTGVAMRSCPEEOYW	40
DPLLGTGCMSCKTICNHOSORTCAAFCSRSLSCRKEQGKFYD	80
HLLRDCISCASICGQHPKQCAYFCENKLSPVNLPPELRR	120
QRSGEVENNSDNSGRYQGLEHRGSEASPALPGLKLSADQV	160
ALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR	200
PRQSPAKSSQDHAMEAGSPVSTSPVPVETCSFCFPECRAP	240
TQESAVTPGTPDPTCAGRWGCHTRTTVLQPCPHIPDSGLG	280
IVCVPAQEGGPGA	293

b.

K-D



c.

TACI

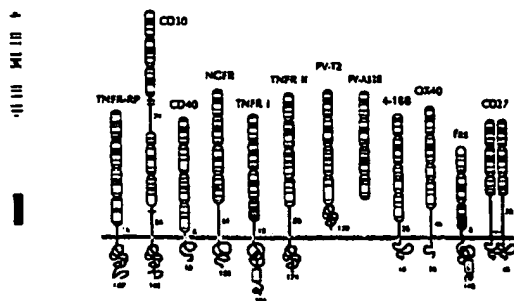
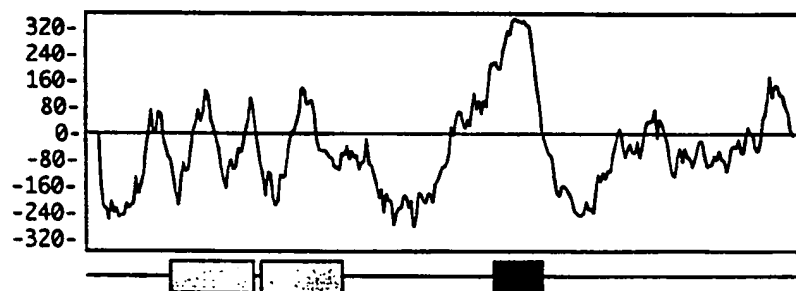


Figure 2

K-D



b.

TACI

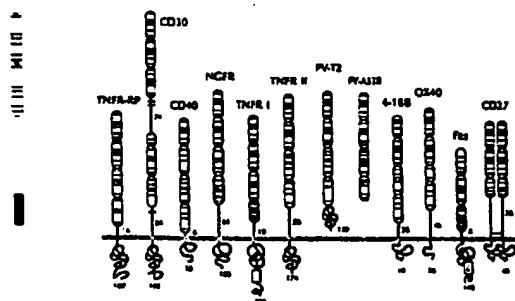


Figure 2

TACI is a signaling prot in resulting in activation of NF-AT-specific transcription.

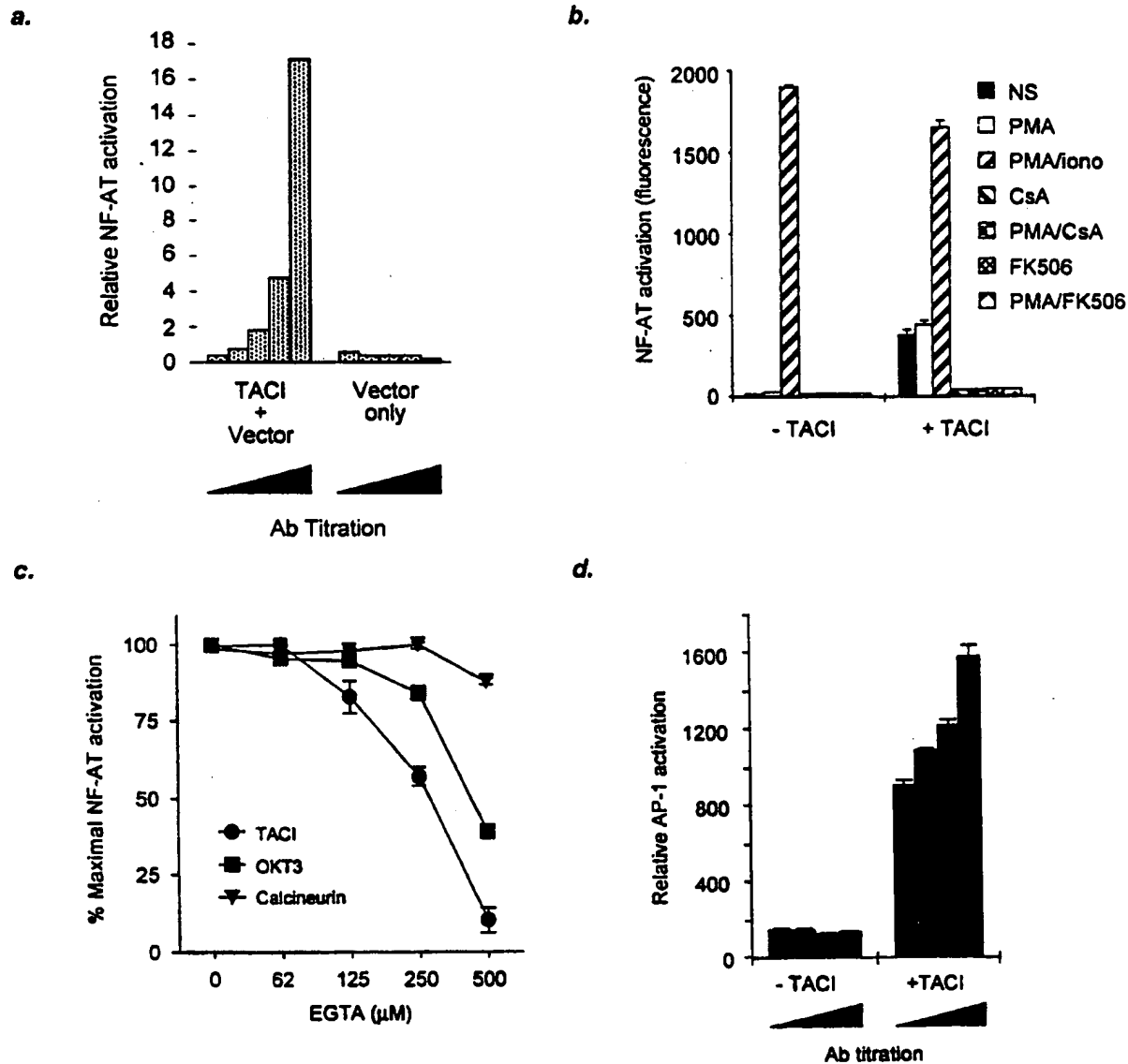


Figure 4

TACI is a signaling protein resulting in activation of NF-AT-specific transcription.

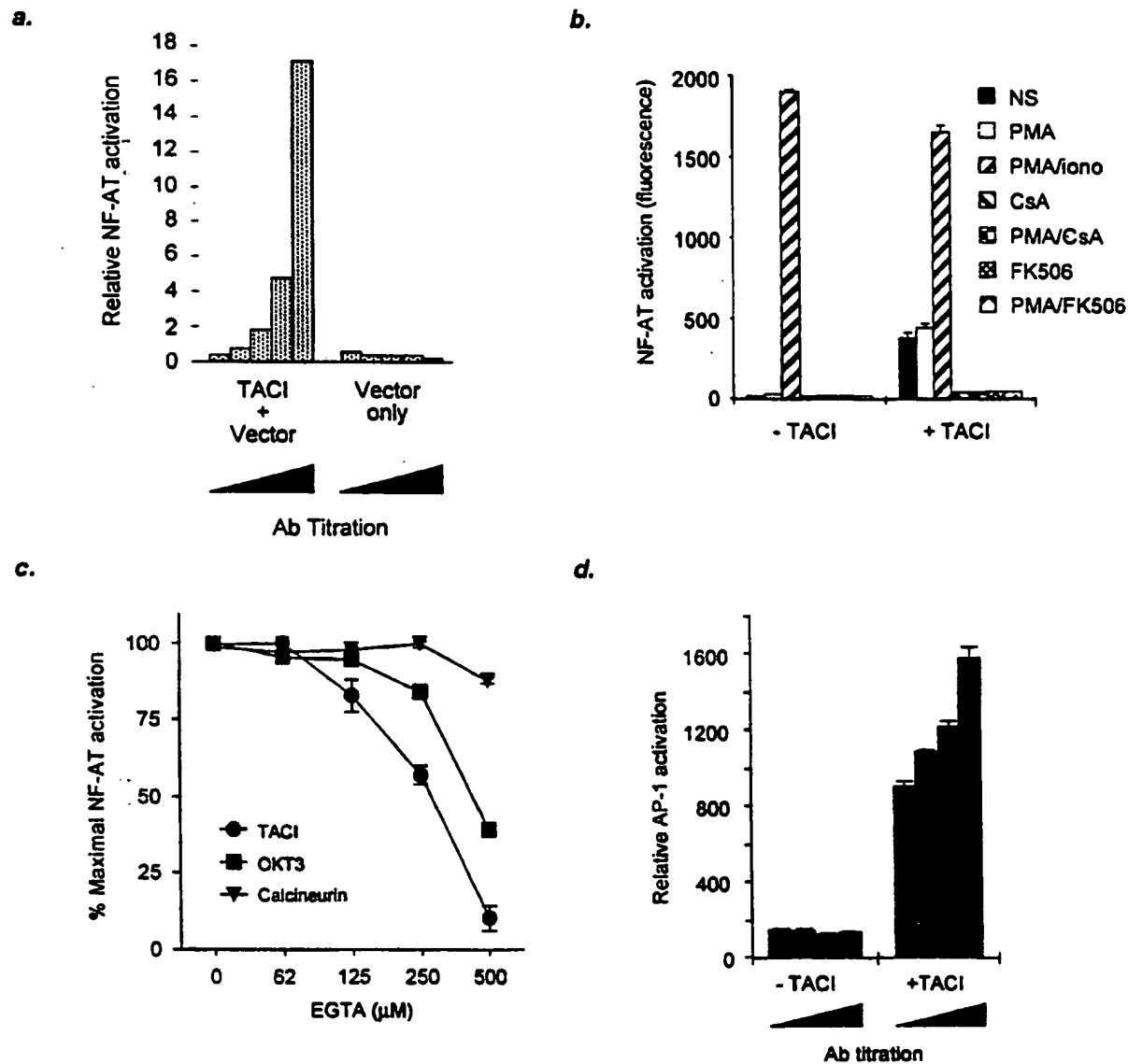


Figure 4

INTERNATIONAL SEARCH REPORT

In. .ational Application No

PCT/US 98/04270

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C07K14/705 C07K16/28 C12N15/12 C12N15/11 C12N5/12
C12N5/10 C12N1/21 C12N1/19 G01N33/68 A01K67/027

According to International Patent Classification(IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A01K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 96 18641 A (YEDA RES & DEV) 20 June 1996 see page 7, paragraph 4-5 see page 15, paragraph 2 see example 3 (i) and (ii): pages 30-34. ---	
A	WO 95 35501 A (UNIV LELAND STANFORD JUNIOR) 28 December 1995 see the whole document and specially example 2. & US 5 523 227 A (R.J. BRAM) 4 June 1996 cited in the application --- -/--	1-9



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Date of the actual completion of the international search

29 July 1998

Date of mailing of the international search report

21/08/1998

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INTERNATIONAL SEARCH REPORT

In. .ational Application No

PCT/US 98/04270

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C12N5/10 C12N1/21 C12N1/19 G01N33/68 A01K67/027

According to International Patent Classification (IPC) or to both national classification and IPC

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Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K A01K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

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A	WO 95 35501 A (UNIV LELAND STANFORD JUNIOR) 28 December 1995 see the whole document and specially example 2. & US 5 523 227 A (R.J. BRAM) 4 June 1996 cited in the application --- -/-	1-9

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International Application No

PCT/US 98/04270

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	M.P. HOLLOWAY AND R.J. BRAM: "A hydrophobic domain of Ca ²⁺ -modulating cyclophilin ligand modulates calcium influx signalling in T lymphocytes" THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 271, no. 15, 1996, pages 8549-8552, XP002072291 BETHESDA, MA, US cited in the application see the whole document ---	1-9
A	K. TASHIRO ET AL., : "Signal sequence trap: a cloning strategy for secreted proteins and type I membrane proteins" SCIENCE, vol. 261, 1993, pages 600-603, XP000673204 WASHINGTON DC, US see the whole document ---	11
P,X	G-U. VON BULOW AND R.J. BRAM: "NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily" SCIENCE, vol. 278, no. 5335, 3 October 1997, pages 138-141, XP002072292 WASHINGTON DC, US see the whole document ---	1-10, 12-22, 26, 29-37,39
P,X	G. U. VON BULOW AND R.J. BRAM: "Activation of the transcription factor NFAT by a novel CAML-interacting member of the tumor necrosis factor" BLOOD, vol. 90, no. 10 suppl. 1 part 1, 15 November 1997, pages 246A-247, XP002072293 NEW YORK, NY, US see the whole document ---	1,5,7,9
P,X	DATABASE NUCLEOTIDE PROTEIN SEQUENCE, - 6 January 1998 XP002072294 HINXTON, GB AC= AC003958, Homo sapiens chromosome 17, clone hRPC.18_F_17. Whitehead Institute/MIT Center for Genome Research, Cambridge, US -----	3

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